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File 351:Derwent WPI 1963-2002/UD,UM &UP=200272
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  File   8:Ei Compendex(R) 1970-2002/Nov W1
         (c) 2002 Elsevier Eng. Info. Inc
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removal, customized scheduling. See HELP ALERT.
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removal, customized scheduling. See HELP ALERT.
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         (c) format only 2002 The Dialog Corporation
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*File 347: JAPIO data problems with year 2000 records are now fixed.
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-key terms

Set   Items   Description
S1   106489   (NANOPARTICLE? ? OR MICROPARTICLE? ? OR PARTICLE? ? OR QUA-
            NTUM(W)DOT? ?) AND (MICROBEAD? ? OR BEAD? ? OR CARRIER? ?)
S2   765   S1 AND LIBRAR?

S12   68   S2 AND REPORTER? ?

S14   57   RD S12 (unique items)
>>>No matching display code(s) found in file(s): 129, 229, 453, 624

 14/3,AB/1   (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI
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014822572
WPI Acc No: 2002-643278/200269
XRAM Acc No: C02-181601
  Protein comprising a variant of model C-type lectin-like domains (CTLD),
  in which alpha helices, beta-strands, connecting segments are conserved
  to maintain CTLD scaffold structure, while the loop region is altered
Patent Assignee: BOREAN PHARMA AS (BORE-N)
Inventor: ETZERODT M; GRAVERSEN N J H; HOLTET T L; THOGERSEN H C
Number of Countries: 100 Number of Patents: 002
Patent Family:
Patent No   Kind   Date   Applicat No   Kind   Date   Week
WO 200248189   A2 20020620 WO 2001DK825   A   20011213 200269 B

AU 200221568 A 20020624 AU 200221568 A 20011213 200269

Priority Applications (No Type Date): US 2001272098 P 20010228; DK 20001872 A 20001213
Patent Details:
Patent No Kind Lan Pg Main IPC Filing Notes
WO 200248189 A2 E 168 C07K-014/47
Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW
AU 200221568 A C07K-014/47 Based on patent WO 200248189

Abstract (Basic): WO 200248189 A2
Abstract (Basic):

NOVELTY - A protein (I) with scaffold structure of C-type lectin-like domains (CTLD), and comprising a variant of a model CTLD where alpha-helices and beta-strands and connecting segments are conserved such that scaffold structure of C-type lectin-like domains (CTLD) is substantially maintained, while the 14loop region is altered by amino acid substitution, deletion, insertion or their combination, is new.

DETAILED DESCRIPTION - A protein (I) has the scaffold structure of C-type lectin-like domains (CTLD), and comprises a variant of a model CTLD where the alpha-helices and beta-strands and connecting segments are conserved to such a degree that the scaffold structure of the CTLD is substantially maintained, while the 14 loop region is altered by amino acid substitution, deletion, insertion or their combination, with the proviso that the protein is not any of the known CTLD loop derivatives of C-type lectin-like proteins or C-type lectins as given in the specification.

INDEPENDENT CLAIMS are also included for the following:

(1) a combinatorial *library"** (II) of (I) having the scaffold structure of CTLD, the proteins comprising variants of model CTLD, where the alpha-helices and beta-strands are conserved to such a degree that the scaffold structure of the CTLD is substantially maintained, while the loop region or parts of the loop region of the CTLD is randomized with respect to amino acid sequence and/or number of amino acid residues;

(2) a derivative (D) of native tetranectin, where upto 10 (more preferably 1-2) amino acid residues are substituted or deleted or inserted in the alpha helices and/or beta strands and/or connecting segments of its CTLD with the proviso that the derivative is not any of the known CTLD derivatives of human tetranectin (hTN) as given in the specification;

(3) nucleic acid sequence (III) comprising a nucleotide sequence encoding a htlec, htCTLD, mtlec, or mtCTLD insert comprising nucleotides 20-562, 20-430, 20-562, or 20-430 of a fully defined sequence of 570 (S12), 438 (S14), 570 (S35) or 438 (S37) nucleotides, respectively as given in the specification;

(4) nucleic acid (IV) comprising a nucleotide sequence encoding (I);

(5) a *library"** of nucleic acids (V) encoding proteins of (II) in which the members of the ensemble of nucleic acids that collectively constitute the *library"** of nucleic acids, are able to be expressed

in a display system, which provides for a logical, physical or chemical link between entities displaying phenotypes representing properties of the displayed expression products and their corresponding genotypes;

(6) preparation of (I);

(7) preparing (II);

(8) constructing a tetranectin derivative adapted for the preparation of (II), where the nucleic acid encoding the tetranectin derivative has been modified to generate endonuclease restriction sites within nucleic acid segments encoding beta2, beta3 or beta4, or upto 30 nucleotides upstream or downstream in the sequence from any nucleotide which belongs to a nucleic acid segment encoding beta2, beta3 or beta4;

(9) use of a nucleotide sequence (N1) encoding a tetranectin, or its derivative where the scaffold structure of its CTLD is substantially maintained, for preparing a *library"** of nucleotide sequences encoding related proteins by randomizing part or all of the nucleic acid sequence encoding the loop region of its CTLD;

(10) screening (II) for binding to a specific target involves:

(a) expressing (V) to display the *library"** of proteins in the display system;

(b) contacting the collection of entities displayed with a suitably tagged target substance for which isolation of a CTLD-derived exhibiting affinity for the target substance is desired;

(c) harvesting subpopulations of the entities displayed that exhibit affinity for the target substance by means of affinity-based selective extractions, utilizing the tag to which the target substance is conjugated or physically attached or adhering to as a vehicle or means of affinity purification, a procedure commonly referred to in the field as affinity panning, followed by re-amplification of the sub-*library"**;

(d) isolating progressively better binders by repeated rounds of panning and re-amplification until a suitably small number of good candidate binders is obtained;and

(e) if desired, isolating each of the good candidates as an individual clone and subjecting it to ordinary functional and structural characterization in preparation for final selection of one or more preferred product clones;

(11) reformatting (I) or a protein selected from (II), and containing a CTLD variant exhibiting desired binding properties, in a desired alternative species-compatible framework by excising the nucleic acid fragment encoding the loop region-substituting polypeptide and any required single framework mutations from the nucleic acid encoding the protein using PCR technology, site directed mutagenesis or restriction enzyme digestion and inserting the nucleic acid fragment into the appropriate location(s) in a display- or protein expression vector that harbors a nucleic acid sequence encoding the desired alternative CTLD framework.

USE - (N1) is useful for preparing a *library"** of nucleotide sequences encoding related proteins by randomizing part or all of the nucleic acid sequence encoding the loop region of its CTLD (claimed).

The artificial CTLD protein products can be employed in applications in which antibody products are presently used as key reagents in technical biochemical assay systems or medical in vitroor in vivo diagnostic assay systems or as active components in therapeutic compositions. The CTLD binding molecule may readily be utilized as a building block for the construction of modular molecular assemblies, e.g., harboring multiple CLTDs of identical or nonidentical specificity in addition to appropriate *reporter"** modules like peroxidases, phosphatases or any other signal mediating moiety. The CTLDs are suited

to serve as a basis for constructing new and useful protein products with desired binding properties.

ADVANTAGEThe artificial CTLD protein products are preferable to antibody derivatives as each binding site in a single structurally autonomous protein domain. When used as components of compositions to be used for in vivo diagnostic or therapeutic purposes, artificial CTLD protein products constructed on the basis of human CTLDs are virtually identical to the corresponding natural CTLD protein already present in the body and are therefore less immunogenic to the patient. They also have a smaller size, and thus provide tissue penetration and distribution, as well as shorter half life in circulation. Since murine and human tetranectin are identical in structure, straightforward swapping of polypeptide segments defining ligand-binding specificity between murine and human tetranectin derivatives may be achieved.

pp; 168 DwgNo 0/35

14/3,AB/2 (Item 2 from file: 351)
DIALOG(R)File 351:Derwent WPI

014787821
WPI Acc No: 2002-608527/200265
XRAM Acc No: C02-172128
Chemical or biological analysis, for diagnosing a disease or screening candidate drugs for treating a disease, by allowing species to participate in a chemical or biological interaction and identifying an oligonucleotide identifier
Patent Assignee: MINERVA BIOTECHNOLOGIES CORP (MINE-N)
Inventor: BAMBAD R S; BAMDAD C C
Number of Countries: 098 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200261129	A2	20020808	WO 2001US45845	A	20011115	200265	B

Priority Applications (No Type Date): US 2001327089 P 20011003; US 2000248863 P 20001115; US 2000252650 P 20001122; GB 20011054 A 20010115; US 2001276995 P 20010319; US 2001302231 P 20010629; US 2001326937 P 20011003
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200261129	A2	E	73	C12Q-001/68	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

Abstract (Basic): WO 200261129 A2
Abstract (Basic):

NOVELTY - Chemical or biological analysis, by allowing a species, immobilized relative to a surface, to participate in a chemical or biological interaction, and determining participation of the chemical or biological species in the chemical or biological interaction by identifying an oligonucleotide identifier that encodes the chemical or biological species associated with the surface, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the

following:
(1) a kit comprising:
(a) an article having a surface;
(b) a chemical or biological species, able to participate in a chemical or biological interaction, fastened to or adapted to be fastened to the surface; and
(c) an oligonucleotide identifier fastened to or adapted to be fastened to the surface;
(2) a kit comprising several *particles"** each carrying a chemical or biological functionality allowing it to fasten to a binding partner, and each carrying an identical oligonucleotide linker constructed for attachment to a complementary oligonucleotide fastened to an oligonucleotide identifier;
(3) a kit comprising:
(a) a surface;
(b) a protein immobilized or adapted to be immobilized relative to the surface; and
(c) an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to the surface;
(4) a kit comprising:
(a) a polymer or dendrimer;
(b) a protein immobilized or adapted to be immobilized relative to the polymer or dendrimer; and
(c) an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to the polymer or dendrimer;
(5) a kit comprising:
(a) a protein and an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to each other; and
(b) an entity carrying immobilized to it a binding partner of the protein;
(6) a kit comprising:
(a) at least one colloid *particle"**;
(b) at least one magnetic *bead"**;
(c) at least one protein recognition motif adapted for immobilization to at least one colloid *particle"**; and
(d) an uncharacterized protein or drug adapted for immobilization to at least one *bead"**;
(7) a composition comprising:
(a) a chemical or biological species, able to participate in a chemical or biological interaction, or a protein;
(b) a linker species that is not a ribosome; and
(c) an oligonucleotide identifier, where each of the chemical or biological species and the oligonucleotide identifier is fastened to or adapted to be fastened to the linker species, or an oligonucleotide identifier that encodes for the protein, where each of the protein and the oligonucleotide identifier is immobilized or adapted to be immobilized relative to the linker species;
(8) a composition comprising a protein and an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to each other;
(9) a method comprising expressing a protein with an oligonucleotide and immobilizing the protein and the oligonucleotide relative to each other;
(10) generating a *library"** of nucleic acids or plasmids that contain components of a cDNA *library"** and:
(a) a functionality to facilitate binding to a surface;

(b) a functionality the products of which are used in an in vitro assay;
(c) sequences to which nucleic acid binding proteins bind; or
(d) sequences that encode a DNA binding domain and sequences to which the encoded DNA binding domain binds, where the binding motif sequences are not in proximity to a *reporter"** gene;
(11) exposing several colloid *particles"**, each carrying an immobilized protein recognition motif, to a *bead"** carrying an immobilized, uncharacterized protein or drug, and determining immobilization of at least one *particle"** to the *bead"** via interaction between the protein recognition motif and the uncharacterized protein or drug.
USE - The methods are useful for chemical and biological analyses, analyzing for the presence of species associated with a disease, diagnosing a disease, or screening of candidate drugs for treating e.g. neurodegenerative diseases.
ADVANTAGE - The present methods are simple, extremely sensitive and utilize readily-available components. The present methods, assays and components provide rapid, high throughput, specific and sensitive detection and analysis of biomolecular and chemical interactions. Large numbers of interactions can be screened simultaneously, as opposed to prior techniques.
pp; 73 DwgNo 0/19

14/3,AB/3 (Item 3 from file: 351)
DIALOG(R)File 351:Derwent WPI

014778750
WPI Acc No: 2002-599456/200264
XRAM Acc No: C02-169287
Isolating peptide domains (PD)s, useful for modulating angiogenesis, by utilizing PD display *library"** which may be used in both display mode attached to microorganism surface, and in secretion mode such that PDs are secreted in soluble form
Patent Assignee: GPC BIOTECH INC (GPCB-N)
Inventor: GYURIS J
Number of Countries: 095 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200246213	A2	20020613	WO 2001US51389	A	20011107	200264	B
AU 200241801	A	20020618	AU 200241801	A	20011107	200266	

Priority Applications (No Type Date): US 2000246461 P 20001107
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200246213	A2	E	98	C07K-014/00	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200241801	A		C07K-014/00	Based on patent WO 200246213

Abstract (Basic): WO 200246213 A2
Abstract (Basic):

NOVELTY - Isolating peptide domain (PD) that modulates angiogenic activity comprising utilizing a PD display *library"**, is new.

DETAILED DESCRIPTION - Isolating (M1) a peptide domain (PD) capable of modulating angiogenic activity, comprising:

(i) providing a first PD display *library"** comprising a variegated population of test PDs expressed on the surface of a population of display packages;

(ii) in a display mode, isolating, from the PD display *library"**, a sub-population of display packages enriched for test PDs which have a binding specificity for an endothelial cells (EC) or its component;

(iii) in a secretion mode, simultaneously expressing the enriched test PD sub-population under conditions where the test PDs are secreted and are free of the display packages;

(iv) assessing the ability of the secreted test PDs to regulate a biological process of an EC; and

(v) assessing the ability of the test PDs capable of regulating a biological process of an EC for the ability to regulate angiogenesis, thereby identifying a PD capable of modulating angiogenic activity, is new.

INDEPENDENT CLAIMS are also included for the following:

(1) a PD display *library"** (II) enriched for test PDs having a binding specificity and/or affinity for an EC or its component and which inhibit EC proliferation and/or migration in a target EC;

(2) a vector (III) comprising a chimeric gene (IIIa) for a chimeric protein, which chimeric gene comprises:

(i) a coding sequence for a test PD;

(ii) a coding sequence for a surface protein of a display package; and

(iii) RNA splice sites flanking the coding sequence for the surface protein, where in a display mode, the chimeric gene is expressed as a fusion protein including the test PD and the surface protein such that the test PD can be displayed on the surface of a population of display packages, where in the secretion mode, the test PD is expressed without the surface protein as a result of the coding sequence for the surface protein being removed by RNA splicing;

(3) a vector *library"** (IV), where each vector comprises (IIIa), and (IV) collectively encodes a variegated population of test PDs4) a cell composition comprising a population of cells containing (IV);

(5) modulating (M2) angiogenic process in an animal by administering a pharmaceutical composition comprising one or more test PD or its peptidomimetics which regulate biological process in target cell, formulated in a *carrier"**, where the test PDs are identified by (M1);

(6) a construct such as pAM7 and pAM9 M13/COS peptide expression plasmid; and

(7) conducting a pharmaceutical business, comprises:

(i) identifying one or more PDs which are capable of modulating angiogenic activity by (M1);

(ii) conducting therapeutic profiling of the identified PD(s), or other homologs or peptidomimetics, for using the PD(s) to modulate angiogenesis; and

(iii) formulating a pharmaceutical preparation including one or more identified PD(s) as a product having an therapeutic profile, or licensing to a third party, the rights for further development of agents to modulate angiogenesis.

ACTIVITY - Vasotropic; Vulnerary; Antiulcer; Antiarthritic; Antidiabetic; Cytostatic; Antiangiogenic. No supporting data is given.

MECHANISM OF ACTION - Angiogenesis modulator. Inhibition of bovine

capillary endothelial (BCE) cell proliferation in transwells by peptide domains identified by (M1) was tested. COS-7 cells were transfected with pAM9-myc, pAM90RGD and pAM9-K1 plasmids, respectively, that direct the expression and secretion of the Myc epitope-6xHis, the Arg-Gly-Asp (RGD) and the angiostatin first kringle domain peptide domains. The transfected COS-7 cells were co-incubated in transwells with BCE cells whose proliferation was stimulated by 1 ng/ml basic fibroblast growth factor (bFGF). As controls, untransfected COS-7 cells and bFGF stimulated BCE cells were similarly co-incubated and synthetic Myc-6xHis and RGD peptide domains as well as purified K1 were added to the media. The proliferation of the bFGF stimulated BCE cells were measured 72 hours later. The synthetic RGD peptide domain and the purified K1 as well as the COS-7 secreted RGD and K1 peptide domains inhibited bFGF stimulated BCE cell proliferation (positive controls). The negative control Myc epitope-6x His peptide did not have inhibitory effect on BCE proliferation.

USE - For isolating a peptide domain capable of modulating angiogenic activity i.e., stimulating or inhibiting angiogenesis. (M1) is most preferably useful for isolating a peptide domain capable of inhibiting angiogenic activity, where in step (iv) the ability of the secreted test peptide domain to inhibit EC proliferation and/or migration is assessed and in step (v) the ability of the test peptides capable of inhibiting EC migration and/or proliferation, to inhibit angiogenesis. (M2) is useful for modulating angiogenic process in an animal (claimed). (M2) is preferably useful for modulating angiogenesis by modulating EC proliferation and/or migration, e.g., (M2) is useful for treating patient suffering from ischemia, wound, ulcers, etc., which require increased angiogenesis or neovascularization and for treating patients suffering from arthritis, diabetes, cancer, etc., in which prevention of new blood vessel formation or reduction in the number of existing blood vessels, is desired.

ADVANTAGE - The display mode and secretion mode can be carried out without the need to sub-clone the test PD coding sequence into another vector. The ability to reduce loss of PD sequences from the sub-*library"** by eliminating sub-cloning steps.

pp; 98 DwgNo 0/9

14/3,AB/4 (Item 4 from file: 351)
DIALOG(R)File 351:Derwent WPI

014688091
WPI Acc No: 2002-508795/200254
XRAM Acc No: C02-144721
Protein-protein complexes for screening drugs or agents that modulate interaction of proteins, e.g. for identifying the Selected Interacting Domains (SID), comprises interaction between beta-TrCP and Ras SF1
Patent Assignee: HYBRIGENICS (HYBR-N); INSERM INST NAT SANTE & RECH MEDICALE (INRM); INST NAT SANTE & RECH MEDICALE (INRM)
Inventor: BENAROUS R; BLOT G; LASSOT I; LEGRAIN P
Number of Countries: 099 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200250261	A2	20020627	WO 2001EP15414	A	20011218	200254	B
AU 200240889	A	20020701	AU 200240889	A	20011218	200264	

Priority Applications (No Type Date): US 2000256276 P 20001218

Patent Details:
Patent No Kind Lan Pg Main IPC Filing Notes
WO 200250261 A2 E 84 C12N-015/00
Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZM ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW
AU 200240889 A C12N-015/00 Based on patent WO 200250261

Abstract (Basic): WO 200250261 A2
Abstract (Basic):

NOVELTY - A complex of protein-protein interaction between betaTrCP and Ras SF1, is new, where the betaTrCP (not defined) comprises 219 amino acids, given in the specification, and the Ras SF1 has 270 amino acids also given in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a complex of polynucleotides between betaTrCP and Ras SF1, which encodes for the polypeptides, comprising 659 base pairs (bp: I) and 1680 bp (II), respectively, given in the specification;

(2) a recombinant host cell expressing the interacting polypeptides of the human placenta (HGXYPLARP1), human undifferentiated PAZ6 adipocytes (HGXYPZURP1) and human differentiated PAZ6 adipocytes (HGXYPZDRP1) *libraries"**, described in the specification;

(3) selecting a modulating compound;

(4) a modulating compound obtained by the method of (3);

(5) a vector comprising the polynucleotide of (1);

(6) a fragment or variant of the polypeptide;

(7) a fragment or variant of the polynucleotide;

(8) a recombinant host cell containing the vectors;

(9) pharmaceutical compositions comprising the vectors, modulating compound or recombinant host cells, and a pharmaceutical *carrier"**;

(10) a protein chip comprising the polypeptides of (6);

(11) a monoclonal antibody of the protein complex;

(12) a truncated Ras SF1A protein lacking amino acids 1 - 19, or a truncated Ras SF1C protein lacking amino acids 1 - 49;

(13) a truncated betaTrCP protein comprising amino acids 260 - 291 of betaTrCP fused to the N-terminal portion of the betaTrCP which precedes the seven WD repeats located at the C-terminus.

ACTIVITY - Cytostatic. No suitable biological data is given.

MECHANISM OF ACTION - Gene therapy.

USE - The protein-protein complex is useful for screening drugs or agents that modulate interaction of proteins. In particular, the protein complex is useful for identifying the Selected Interacting Domains (SID (RTM)). The modulating compounds detected can be used for treating tumors. The polynucleotides encoding the protein complex may used in gene therapy.

pp; 84 DwgNo 0/20

14/3,AB/5 (Item 5 from file: 351)
DIALOG(R)File 351:Derwent WPI

014669780

WPI Acc No: 2002-490484/200252
XRAM Acc No: C02-139318
Rapid screening for biological effectors, useful as diagnostic or therapeutic agents, by testing identifiable *library"** components on a particulate system
Patent Assignee: PHYLOS INC (PHYL-N); AVENTIS RES & TECHNOLOGIES GMBH & CO KG (AVET)
Inventor: POLAKOWSKI T; SCHNEIDER E; SOLSBACHER J; WAGNER P
Number of Countries: 099 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200246397	A1	20020613	WO 2001EP14337	A	20011206	200252	B
DE 10060959	A1	20020620	DE 1060959	A	20001206	200252	
AU 200216076	A	20020618	AU 200216076	A	20011206	200262	

Priority Applications (No Type Date): DE 1060959 A 20001206
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200246397	A1	G	27	C12N-015/10	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

DE 10060959	A1		C12Q-001/68	
AU 200216076	A		C12N-015/10	Based on patent WO 200246397

Abstract (Basic): WO 200246397 A1
Abstract (Basic):
NOVELTY - Isolating and identifying effectors (I), i.e. agents that bind to components of a particulate system (A) and have a biological effect, is new. (A) are exposed to a *library"** of components, to which individual nucleic acids (NA) can be assigned, and the biological effect in and/or on the (I)-laden system is used to isolate (I)-laden systems, by cell sorting and/or by growth selection.
DETAILED DESCRIPTION - Isolating and identifying effectors (I), i.e. agents that bind to components of a particulate system (A) and have a biological effect, is new. (A) are exposed to a *library"** of components, to which individual nucleic acids (NA) can be assigned, and the biological effect in and/or on the (I)-laden system is used to isolate (I)-laden systems, by cell sorting and/or by growth selection. The identity of (I) is determined by identifying the assigned NA, or part of it.
INDEPENDENT CLAIMS are also included for the following:
(1) (I) isolated this way; and
(2) diagnostic and pharmaceutical compositions containing (I) or parts of them.
USE - (I) and their fragments are potentially useful as diagnostic and therapeutic agents.
ADVANTAGE - The method provides high throughput screening of effectors present in complex mixtures, without the compartmentalization required in known systems. The complex mixture can be screened for many different effectors simultaneously and *libraries"** of up to 10 to the power 15 components can be screened within a few weeks.
pp; 27 DwgNo 0/0

14/3,AB/6 (Item 6 from file: 351)
DIALOG(R)File 351:Derwent WPI

014669510
WPI Acc No: 2002-490214/200252
XRAM Acc No: C02-139240
XRPX Acc No: N02-387494
Chemical-*library"** composition useful for multiplexed detection and quantification of analyte comprises several coded *carriers"** and a different known compound carried on each *carrier"**
Patent Assignee: VIRTUAL ARRAYS INC (VIRT-N)
Inventor: GOLDBARD S; HYUN W C; RAVKIN I; ZAROWITZ M A
Number of Countries: 097 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200242736	A2	20020530	WO 2001US51270	A	20011019	200252	B
AU 200239775	A	20020603	AU 200239775	A	20011019	200263	

Priority Applications (No Type Date): US 2000694077 A 20001019
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200242736	A2	E	87	G01N-000/00	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200239775	A		G01N-000/00	Based on patent WO 200242736	

Abstract (Basic): WO 200242736 A2
Abstract (Basic):

NOVELTY - A chemical-*library"** composition (I) comprising several coded *carriers"**, and a different known chemical carried on each different-combination *carrier"**, is new. Each *carrier"** has N more than 1 spatial code position and one of M more than 2 optically detectable indicia at each code position. Each *carrier"** is optionally identified by up to M to the power N different code combinations. Each of the M more than 2 indicia is a different color.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

(1) forming *library"** of determinable chemical compounds, comprising:

(a) placing into each of the several separate reaction vessels, *carriers"** having selected one of several optically detectable code combinations, each *carrier"** is defined by one of N more than 1 spatial code positions and one of M more than 2 optionally detectable indicia at each spatial code position, such that each *carrier"** in any vessel, have one of M to the power N different code combinations;

(b) reacting the *carriers"** in each vessel with reagents to form the *carriers"**, as solid-supports, a selected one of M to the power N different known *library"** compounds; and

(c) forming a mixture of *carriers"** from different reaction vessels;

(2) detecting at least one target molecule capable of binding to at least one different known *library"** compounds involving:

(a) contacting the target molecules with (I);
(b) distributing the *carriers"** for individual-*carrier"** decoding;
(c) detecting *carriers"** having bound target molecules; and
(d) decoding the *carriers"** having bound target molecules to identify the *library"** compounds to which the target molecules are bound;
(3) multiplexing the detection and quantification of analytes, comprising:
(a) distributing on a surface several coded *carriers"**;
(b) scanning the surface for *carriers"** having detectable *reporter"**;
(c) recording the positions of the *carriers"** having a detectable *reporter"**; and
(d) determining the code for each *carrier"** at each recorded position, each *carrier"** has different compound attached to it4) an array device comprising a surface and several spatially coded *carriers"** having different compounds attached to different *carriers"**, the *carriers"** have N more than 1 spatial code positions and M more than 2 optically coding indicia at each spatial coding position, each of the optical coding indicia has different color, the *carriers"** are randomly distributed upon the surface;
(5) a kit comprising several separated classes of compoundless coded *carriers"**, each class contains several *carriers"**, each *carrier"** in the class has spatial code, the spatial code has N more than 1 spatial coding position and M more than 2 optical indicia at each coding position, each optical indicia is of different color, the different class has compoundless coded *carriers"** having different code, each *carrier"** has a compound attached to it;
(6) preparing (I) comprising forming thin transverse section of an assembly comprising N more than 1 filament regions of M more than 2 different colors by bundling together the filaments to form fused bundle and sectioning the fused bundle to produce *carriers"** having one of M more than 2 color indicia at each of the N more than 1 spatial code position and attaching to each of the *carriers"** a different known chemical;
(7) detecting at least two target molecules in an analyte capable of binding to at least two known different compounds on different *carriers"** from a *carrier"** *library"** contained in a sample, comprising:
(a) partitioning the *carrier"** *library"** into several sublibraries and splitting the analyte into several subanalytes;
(b) contacting each subanalyte with a sublibrary where at least one target molecule can bind to at least one corresponding sublibrary *carrier"**;
(c) pooling together *carriers"** from all sublibraries;
(d) distributing the *carriers"** on substrate;
(e) detecting *carriers"** having bound target molecules and decoding the *carriers"** having bound target molecules to identify each compound that bound target molecules are bound, the conditions are independent for each sublibrary;
(8) a coded *particle"** (B) for use in carrying out selected reactions or analyses comprising several self-oriented coded *carriers"** and a different known chemical carried on each different-combination *carrier"**, each *carrier"** has N more than 1 spatial code compartments and one of M more than 2 optically detectable indicia at each code compartment, each *carrier"** can be optically identified by one of up to M to the power N different code

combinations, each of the M more than 2 indicia has different color, each *carrier"** is formed of N separate layers or bundled fibers, each layer or bundled fiber has one of M different color indicia, the layers or bundled fibers form the spatial code compartments, the *carrier"** is formed in a shape to adapt to self orient into a *carrier"** holder within a holder array to expose the spatial code to an optical window within the holder9) apparatus for detecting activity on (B) and determining the code comprising a *carrier"** holder array, the *carrier"** has several holders distributed within it, the holders hold the *carrier"** so that the coded *carrier"** code faces an optical window connected to a detector, the surface displays the spatial code, the *carrier"** is held in the holder after the *carrier"** is positioned within the holder, the detector detects an activity on the *carrier"** and the detector also detects the spatial code of the *carrier"**;

(10) *microparticle"** for identifying at least one compound attached to it comprising the coded *carrier"** and at least one known compound attached to the *carrier"**, the compound has at least one identifying feature, the code correlates to it; and

(11) an apparatus for analyzing event occurring on or adjacent a *microparticle"** containing an identifying code having a code viewing surface comprising a fiber optic receiver, a detector and a reader, the receiver has an outer cladding protruding from one end of an inner core to form a wall of a receiver area for receiving and orienting the *microparticle"** so that a code-viewing surface of the identifying code faces the end of the fiber optic receiver, the detector detects the events occurring on or adjacent the coded *microparticle"**, the detector is in optical communication with the inner core, the reader reads the code from a code-viewing surface, the reader is in optical communication with the inner core, the receiver area holds the *particle"** so that the code's viewing surface is readable by the reader, the events are detectable by the detector, whereas the *microparticle"** resides within the receiver area.

USE - For multiplexed analysis of at least one different known cell population, for forming a *library"** of determinable chemical compounds, for detecting at least one target molecule, for multiplexing the detection and quantifying analytes (claimed).

ADVANTAGE - The *carriers"** used in the composition provides more homogenous and reproducible representation for probe molecules and products than the two-dimensional imprinted array or DNA chips. The composition allows multiplexed analysis that does not have the cost prohibition of current microarray products.

pp; 87 DwgNo 0/20

14/3,AB/7 (Item 7 from file: 351)
DIALOG(R)File 351:Derwent WPI

014541721
WPI Acc No: 2002-362424/200239
XRAM Acc No: C02-102646
New SPAS-1 protein or antigen obtained from TRAMP-C2 tumor cells, useful as vaccine for treating or inhibiting cancer in patient, e.g. prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney or germ cell cancer
Patent Assignee: UNIV CALIFORNIA (REGC); ALLISON J P (ALLI-I); FASSO M (FASS-I); SHASTRI N (SHAS-I)

Inventor: ALLISON J P; FASSO M; SHASTRI N
Number of Countries: 023 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200224739	A2	20020328	WO 2001US28621	A	20010913	200239 B
AU 200190860	A	20020402	AU 200190860	A	20010913	200252
US 20020150588	A1	20021017	US 2000234472	A	20000921	200270
			US 2001952432	A	20010913	

Priority Applications (No Type Date): US 2000234472 P 20000921; US 2001952432 A 20010913
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200224739	A2	E	107	C07K-014/435	
Designated States (National): AU CA JP					
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
AU 200190860	A			C07K-014/435	Based on patent WO 200224739
US 20020150588	A1			A61K-039/00	Provisional application US 2000234472

Abstract (Basic): WO 200224739 A2
Abstract (Basic):

NOVELTY - An isolated polypeptide comprising an immunogenic portion of a SPAS-1 protein, or its variant that differs one or more substitutions, deletions, additions or insertions, where the SPAS-1 protein comprises an amino acid sequence that is encoded by a partial (995 base pairs) or full length (1185 base pairs) SPAS-1 cDNA from TRAMP-C2 tumor cells, or their complements, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an isolated SPAS-1 polynucleotide comprising:

(a) the bp sequence cited above;

(b) a polynucleotide that:

(i) hybridizes under stringent hybridization conditions to (a);

(ii) encodes the polypeptide with the sequence having 331 or 395 amino acids fully defined in the specification, or its allelic variant or homologue; or encodes a polypeptide with at least 15 contiguous residues of the amino acid sequence cited above; or

(iii) has at least 15 contiguous bases identical to or exactly complementary the bp sequence cited above;

(c) a polynucleotide encoding at least 15 amino acid residues of a SPAS-1 protein, or its a variant that differs in one or more substitutions, deletions, additions or insertions, where the tumor protein comprises the amino acid sequence cited above or their complement; or

(d) a polynucleotide encoding a SPAS-1 protein or its variant;

(2) a vector comprising the polynucleotide or an expression vector comprising the polynucleotide in which the nucleotide sequence is operatively linked with a regulatory sequence that controls expression of the polynucleotide in a host cell;

(3) a host cell comprising the polynucleotide, or progeny of the cell;

(4) producing the polypeptide;

(5) an isolated antibody or its antigen-binding fragment that specifically binds to at least an immunogenic portion of the SPAS-1 human homolog polynucleotides sequence or its complement;

(6) a fusion protein comprising at least an immunogenic portion of the SPAS-1 human homolog polypeptide sequence;

(7) an isolated polynucleotide encoding the fusion protein;
(8) pharmaceutical compositions comprising a pharmaceutical *carrier"** or excipient, and:
(a) at least an immunogenic portion of the SPAS-1 human homolog polynucleotides sequence (GenBank Accession Number AF257319);
(b) the antibody or its fragment;
(c) an antigen-presenting cell that expresses at least an immunogenic portion of the SPAS-1 human homolog polypeptide;
(d) the fusion protein; or
(e) the polynucleotide encoding the fusion protein;
(9) vaccines comprising:
(a) at least an immunogenic portion of the SPAS-1 human homolog polynucleotides sequence or its complements, and/or DNA sequences that hybridize to the SPAS-1 human homolog polynucleotide sequence; and a non-specific immune response enhancer; or
(b) an antigen-presenting cell that expresses at least an immunogenic portion of the SPAS-1 human homolog polypeptide sequence, in combination with a non-specific immune response enhancer;
(10) removing tumor cells from a biological sample by contacting a biological sample with T cells that specifically react with the SPAS-1 human homolog protein;
(11) stimulating T cells specific for the SPAS-1 protein comprising contacting T cells with one or more of the following:
(a) at least an immunogenic portion of the SPAS-1 human homolog polypeptide;
(b) the polynucleotide encoding the SPAS-1 human homolog polypeptide; or
(c) an antigen presenting cell that expresses the SPAS-1 human homolog polypeptide;
(12) an isolated T cell population comprising T cells prepared by the method of (11);
(13) inhibiting the development of a cancer in a patient;
(14) determining the presence or absence of a cancer in a patient;
(15) monitoring the progression of a cancer in a patient; and
(16) a diagnostic kit, comprising:
(a) one or more of the antibodies cited above; and
(b) a detection reagent comprising a *reporter"** group.
ACTIVITY - Cytostatic. No clinical tests described.
MECHANISM OF ACTION - Vaccine.
USE - The immunogenic portion of the SPAS-1 human homolog polynucleotides sequence, the antibody or its antigen-binding fragment, the antigen-presenting cell, the T cell population and the pharmaceutical compositions are useful for inhibiting the development of a cancer in a patient, specifically prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney, chronic lymphocytic leukemia or germ cell cancer (claimed). In particular, these compounds are useful for as vaccines for inducing protective immunity against cancer. The above mentioned compounds or compositions are also useful for diagnosing cancer and monitoring cancer progression. The patients may include humans, dogs, cats, cattle, horses, pigs, monkeys, rabbits, rats or mice.
pp; 107 DwgNo 0/18

14/3,AB/8 (Item 8 from file: 351)
DIALOG(R)File 351:Derwent WPI

014519481
WPI Acc No: 2002-340184/200237
Related WPI Acc No: 1999-095351; 2001-146289; 2001-367710; 2002-017124; 2002-017125; 2002-017215; 2002-194904; 2002-239225
XRAM Acc No: C02-097844
Identifying polynucleotide in liquid phase comprises contacting polynucleotides derived from organism with nucleic acid probe labelled with detectable molecule and identifying polynucleotide
Patent Assignee: DIVERSA CORP (DIVE-N); LAFFERTY W M (LAFF-I)
Inventor: LAFFERTY W M; KELLER M; SHORT J M
Number of Countries: 097 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200231203	A2	20020418	WO 2001US31806	A	20011010	200237 B
US 20020048809	A1	20020425	US 97876276	A	19970616	200245
			US 9898206	A	19980616	
			US 99444112	A	19991122	
			US 2000636778	A	20000811	
			US 2000687219	A	20001012	
			US 2001790321	A	20010221	
AU 200211642	A	20020422	AU 200211642	A	20011010	200254

Priority Applications (No Type Date): US 2001309101 P 20010731; US 2000685432 A 20001010; US 2000738871 A 20001215; US 2001790321 A 20010221 ; US 2001894956 A 20010627; US 97876276 A 19970616; US 9898206 A 19980616 ; US 99444112 A 19991122; US 2000636778 A 20000811; US 2000687219 A 20001012
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200231203	A2	E	228	C12Q-001/68	
Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW				
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
US 20020048809	A1			C12Q-001/68	CIP of application US 97876276 Cont of application US 9898206 CIP of application US 99444112 CIP of application US 2000636778 CIP of application US 2000687219
AU 200211642	A			C12Q-001/68	Based on patent WO 200231203

Abstract (Basic): WO 200231203 A2
Abstract (Basic):

NOVELTY - Identifying a polynucleotide in a liquid phase comprises contacting polynucleotides derived from at least one organism with at least one nucleic acid probe labelled with detectable molecule so that the probe is hybridized to the polynucleotides having complementary sequences and identifying a polynucleotide with an analyzer to detect the detectable molecule.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

(1) identifying a polynucleotide encoding a polypeptide which comprises coencapsulating in a microenvironment a *library"** of clones containing DNA obtained from a mixed population of organisms with a mixture of oligonucleotide probes comprising a detectable label and at least a part of a polynucleotide sequence encoding a polypeptide having a specified bioactivity under conditions and for a time to allow

interaction of complementary sequences and identifying clones containing a complement to the oligonucleotide probe encoding the polypeptide by separating clones with an analyzer to detect the detectable label;

(2) high throughput screening of a polynucleotide *library"** for a polynucleotide that encodes a molecule which comprises contacting a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms with oligonucleotides probes labelled with a detectable molecule and separating clones with an analyzer to detect the molecule;

(3) screening for a polynucleotide encoding an activity which comprises:

(a) normalizing polynucleotides obtained from an environmental sample;

(b) generating a *library"** from the polynucleotides;

(c) contacting the *library"** with oligonucleotide probes comprising a detectable label and at least a part of a polynucleotide sequence encoding a polypeptide having a specified activity to select *library"** clones positive for a sequence and

(d) selecting clones with an analyzer to detect the label;

(4) screening polynucleotides which comprises contacting a *library"** of polynucleotides derived from a mixed population of organisms with a probe oligonucleotide labelled with a fluorescence molecule which fluoresces upon binding of the probe to a target polynucleotide of the *library"** to select *library"** polynucleotides positive for a sequence, separating *library"** members that are positive for the sequence with a fluorescent analyzer to detect fluorescence and expressing the selected polynucleotides to obtain polypeptides;

(5) obtaining an organism from a mixed population of organisms in a sample which comprises encapsulating at least one organism from the sample in a microenvironment, incubating under conditions and for a time to allow the organism to grow or proliferate and sorting the organism by a flow cytometer;

(6) identifying a bioactivity or biomolecule which comprises transferring a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms to a first host cell, contacting the cell with a second host cell containing a detectable *reporter"** molecule in a microenvironment and separating clones with an analyzer to detect the molecule;

(7) identifying a bioactivity or biomolecule which comprises transferring a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms to a first host cell, contacting the cell with a second host cell containing a detectable *reporter"** molecule in a microenvironment and optionally separating clones with an analyzer to detect the molecule;

(8) identifying a bioactivity or biomolecule which comprises transferring the extract of a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms to a first host cell and contacting the extract with a second host cell containing a detectable *reporter"** molecule;

(9) identifying a bioactivity or biomolecule which comprises transferring the extract of a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms through a column, transferring the extract to a first host cell, contacting the extract with a second host cell containing a detectable *reporter"** molecule and measuring the mass spectra of the host cell with the extract;

(10) a sample screening apparatus which comprises an array of capillaries comprising at least one wall defining a lumen for retaining a sample, interstitial material between capillaries and at least one reference indicia formed within the interstitial material;

(11) a capillary for screening a sample which comprises a first wall defining a lumen for retaining the sample and forming a waveguide for propagating detectable signals and a second wall formed of a filtering material for filtering excitation energy to the lumen to excite the sample;

(12) a capillary array for screening samples which comprises capillaries as above;

(13) incubating a bioactivity or biomolecule which comprises introducing a first component into at least a part of a capillary of a capillary array, introducing air into the capillary behind the first component and introducing a second component into the capillary;

(14) incubating a sample which comprises introducing a first liquid labelled with a detectable *particle"** into a capillary of a capillary array, optionally with at least one wall coated with a binding material, submersing one end of the capillary into a fluid bath containing a second liquid and evaporating the first liquid;

(15) incubating a sample which comprises introducing a liquid labelled with a detectable *particle"** into a capillary of a capillary array, introducing paramagnetic *beads"** to the liquid and exposing the capillary containing the *beads"** to a magnetic field;

(16) recovering a sample from one capillary in an array which comprises determining a coordinate position of a recovery tool, detecting a coordinate location of a capillary containing the sample, correlating, via relative movement between the recovery tool and the capillary containing the sample, the coordinate position of the recovery tool with the location of the capillary and contacting the capillary and recovery tool;

(17) a recovery apparatus which comprises a recovery tool to contact at least one capillary and recover a sample and an ejector, connected with the recovery tool, for ejecting the sample from the tool 18) a sample screening apparatus which comprises capillaries in an array, interstitial material and at least one reference indicia formed within the interstitial material, and

(19) enriching a polynucleotide encoding an activity which comprises contacting a mixed population of polynucleotides derived from a mixed population of organisms with at least one nucleic acid probe.

USE - Used for screening for polynucleotides, proteins and small molecules using high throughput of multiple samples.

ADVANTAGE - Rapid sorting and screening of *libraries"** from a mixed population of organisms may be effected.

pp; 228 DwgNo 0/23

14/3,AB/9 (Item 9 from file: 351)
DIALOG(R)File 351:Derwent WPI

014439666
WPI Acc No: 2002-260369/200231
XRAM Acc No: C02-077451
XRPX Acc No: N02-202015

Making microarrays of biological materials e.g. anti-ligands for use in diagnosis, comprises exposing a *library"** of anti-ligands to a mixture of ligands, isolating bound anti-ligands, amplifying, and applying it to

substrate
Patent Assignee: BIOINVENT INT AB (BIOI-N); BORREBAECK C A K (BORR-I); CARLSSON R (CARL-I)
Inventor: BORREBAECK C A K; CARLSSON R
Number of Countries: 095 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
GB 2360282	A	20010919	GB 20006425	A	20000317	200231	B
AU 200152160	A	20010924	AU 200152160	A	20010306	200231	
US 20010053520	A1	20011220	US 2000192256	P	20000327	200231	
			US 2001811075	A	20010316		
WO 200169247	A2	20010920	WO 2001EP2520	A	20010306	200231	

Priority Applications (No Type Date): GB 20006425 A 20000317
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
GB 2360282	A		40	G01N-033/53	
AU 200152160	A			G01N-033/53	Based on patent WO 200169247
US 20010053520	A1			C12Q-001/68	Provisional application US 2000192256
WO 200169247	A2	E		G01N-033/53	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

Abstract (Basic): GB 2360282 A
Abstract (Basic):

NOVELTY - Making (M1) an array of selected anti-ligand molecules (ALs) comprises:

(a) exposing a *library"** (I) of AL molecules to a mixture of ligands (L1s) to allow L1/AL binding;

(b) isolating and amplifying the number of ALs which bind L1s; and

(c) applying a preparation of the same or several different ALs, to a separate region of a substrate to form an array of separate AL-containing regions on a solid support

DETAILED DESCRIPTION - Making (M1) an array of selected anti-ligand molecules (ALs) comprises:

(i) providing a *library"** (I) of AL molecules displayed for binding with a ligand (L1) on the surface of a replicable unit;

(ii) providing a mixture of L1s;

(iii) exposing (I) to the mixture where L1/AL binding can take place;

(iv) isolating and amplifying the number of ALs which bind L1s; and

(v) applying a preparation of the same or several different ALs, to a separate region of a substrate to form an array of separate AL-containing regions on a solid support.

An INDEPENDENT CLAIM is also included for use of an array or two or more substantially identical arrays obtainable by M1 for comparing the presence, absence and/or amount of one or more L1s in a first biological sample (BS1) and a second biological sample (BS2) by detecting differences in L1/AL binding when an array is exposed to the samples, or one array is exposed to BS1 and a substantially identical array is exposed to BS2.

USE - M1 is useful for making an array of selected ALs where one of the array or two or more substantially identical arrays obtainable by

the method is useful for comparing the presence, absence and/or amount of one or more L1s in BS1 which is from a diseased cell type and BS2s which is from a corresponding cell type unaffected by the disease, and where L1s in BS1 and BS2 are labeled with two different fluorescent *reporters"** so that, in use, under examination of the array under conditions of fluorescence excitation, ALs in the array which are bound predominantly to L1s from one of BS1 and BS2 give a first or second fluorescence emission, and ALs which bind substantially equal numbers of L1s from BS1 and BS2 give a combined fluorescence emission (claimed). The method can be used in diagnosing particular disorders.

ADVANTAGE - Unlike methods which involve excision of individual ligands bands separately from a gel replica, direct use of the gel replica is enormous less time consuming and economical too. Moreover, the identity of at least some, and preferably all, of the ligands and/or anti-ligands may be unknown, and hence, prior characterization of ligands, and/or anti-ligands is unnecessary. Unlike a conventional immunoassay, assay using the microarray produced by M1 has the ability to include a population of antibodies diagnostic for a variety of disorders on a single surface, significantly reducing time, costs and materials needed to effect a diagnosis.

pp; 40 DwgNo 0/0

14/3,AB/10 (Item 10 from file: 351)
DIALOG(R)File 351:Derwent WPI

014350324
WPI Acc No: 2002-171027/200222
Related WPI Acc No: 2001-211395; 2002-500186
XRAM Acc No: C02-052771
Ovarian tumor polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer
Patent Assignee: ALGATE P A (ALGA-I); FLING S P (FLIN-I); STOLK J A (STOL-I); XU J (XUJJ-I)
Inventor: ALGATE P A; FLING S P; STOLK J A; XU J
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
US 20020004491	A1	20020110	US 99394374	A	19990910	200222	B
			US 2000561778	A	20000501		
			US 2000640173	A	20000815		
			US 2000656668	A	20000907		
			US 2000713550	A	20001114		
			US 2001825294	A	20010403		

Priority Applications (No Type Date): US 2001825294 A 20010403; US 99394374 A 19990910; US 2000561778 A 20000501; US 2000640173 A 20000815; US 2000656668 A 20000907; US 2000713550 A 20001114
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
US 20020004491	A1		131	A61K-048/00	CIP of application US 99394374
					CIP of application US 2000561778
					CIP of application US 2000640173
					CIP of application US 2000656668
					CIP of application US 2000713550

Abstract (Basic): US 20020004491 A1

Abstract (Basic):

NOVELTY - An isolated ovarian tumor polypeptide (I) comprising a sequence (S1) of 55, 67, 73, 787, 453 or 141 amino acids fully defined in the specification, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an isolated polynucleotide (II) comprises a sequence selected from:

(a) a sequence (S2) selected from 84 sequences having 396 base pairs (bp), and a sequence of 924, 3321, 487, 3999, 1069, 1817, 2382, 2377, 1370, 2060, 3000, 1409, 447, 707, 552, 449, 606, 369, 2008, 2364, 1362, 625, 1619, 1010, 480 or 1897 bp fully defined in the specification;

(b) complements of (S2);

(c) sequences consisting of at least 20 contiguous residues of (S2);

(d) sequences that hybridize to (S2) under moderately stringent conditions;

(e) sequences having at least 75% preferably 90% identity to (S2); and

(f) degenerate variants of (S2);

(2) an isolated polypeptide (III) encoded by (II) comprises a sequence from a sequence (S1); sequences encoded by (II); and sequences having 70% preferably 90% identity to sequence encoded by (II);

(3) an expression vector (IV) comprising (II) operably linked to a expression control sequence;

(4) a host cell transformed or transfected with (IV);

(5) an isolated antibody (Ab), or its antigen binding fragment specific to (III);

(6) detecting (M1) an ovarian cancer in a patient, comprising contacting a biological sample from the patient with a binding agent that binds to (III), detecting amount of (III) bound to the binding agent, and comparing the amount to a predetermined cut-off value;

(7) a fusion protein (V) comprising (III);

(8) an oligonucleotide (OLI) that hybridizes to (S2) under moderately stringent conditions;

(9) stimulating and/or expanding (M2) T-cells specific for a tumor protein comprising contacting T-cells with (II), (III) or antigen presenting cells (APC) that express (II);

(10) an isolated T-cell population (VI) comprising T-cells prepared by M2;

(11) a composition (C1) comprising *carriers"**, immunostimulants, and (I), (II), Ab, (IV), (V) or APC;

(12) a diagnostic kit comprising OLI, or Ab and detection reagent comprising a *reporter"** group; and

(13) inhibiting (M3) the development of a cancer in a patient comprising incubating CD4+ and/or CD8+ T cells isolated from a patient with (III), (II) or APC, such that T cell proliferate, and administering to the patient the proliferated T cells.

ACTIVITY - Cytostatic.

No biodata is given in the source material.

MECHANISM OF ACTION - Vaccine; Gene therapy.

USE - M1 is useful for detecting a cancer in a patient; M2 is useful for stimulating and/or expanding T-cells specific for a tumor protein; and (M3) is useful for inhibiting the development of a cancer in a patient. C1 is useful for stimulating an immune response in a patient and for treating a cancer in a patient. OLI is useful for determining the presence of a cancer in a patient. The method comprises

contacting biological sample from the patient with OLI, detecting amount of (II) that hybridizes to OLI, and comparing the amount to a predetermined cutoff value (claimed). (VI) is further useful for removing tumor cells from a biological sample. (II) is useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumor polypeptides in tumor cells. (I), (II), (III) or (V) is useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Host cells transformed with (II) is useful for preparation of (I).

pp; 131 DwgNo 0/0

14/3,AB/11 (Item 11 from file: 351)
DIALOG(R)File 351:Derwent WPI

014333986
WPI Acc No: 2002-154689/200220
XRAM Acc No: C02-048365

Novel isolated polypeptide comprising at least an immunogenic portion of herpes simplex virus antigen, useful as component of vaccines used for treating herpes simplex virus infection in a patient

Patent Assignee: CORIXA CORP (CORI-N); DAY C H (DAYC-I); DILLON D C (DILL-I); HOSKEN N A (HOSK-I); MCGOWAN P (MCGO-I); SLEATH P R (SLEA-I)
Inventor: DAY C H; DILLON D C; HOSKEN N A; MCGOWAN P; SLEATH P R
Number of Countries: 096 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200202131	A2	20020110	WO 2001US20981	A	20010628	200220 B
AU 200173128	A	20020114	AU 200173128	A	20010628	200237
US 20020090610	A1	20020711	US 2000215458	P	20000629	200248
			US 2001277438	P	20010320	
			US 2001894998	A	20010628	

Priority Applications (No Type Date): US 2001277438 P 20010320; US 2000215458 P 20000629; US 2001894998 A 20010628
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200202131	A2	E	157	A61K-038/00	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200173128	A		A61K-038/00	Based on patent WO 200202131
US 20020090610	A1		C12Q-001/70	Provisional application US 2000215458
				Provisional application US 2001277438

Abstract (Basic): WO 200202131 A2
Abstract (Basic):

NOVELTY - An isolated polypeptide (I) comprising at least an immunogenic portion of an herpes simplex virus (HSV) antigen which comprises one of 28 22-1142 residue amino acid sequences, fully defined in the specification, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an isolated polynucleotide (II) encoding (I);

(2) a fusion protein (III) comprising (I) and a fusion partner;

(3) an isolated polynucleotide (IV) encoding (III);

(4) an isolated monoclonal or polyclonal antibody or its antigen-binding fragment (V), that specifically binds to (I);

(5) a composition (VII) comprising (I), (II) and a *carrier"**;

(6) a pharmaceutical composition (a vaccine) (VIII) comprising (I), (II) and an immunostimulant;

(7) a diagnostic kit (IX) comprising (I), (III), (V) and a detection reagent;

(8) a pharmaceutical composition (X) for the treating of HSV infection in a patient, comprising T cells proliferated in the presence of (I), in combination with a *carrier"**;

(9) treating (M1) HSV infection in a patient by incubating antigen presenting cells (APC) in the presence of (I), which are then administered to the patient; and

(10) a pharmaceutical composition (XI) for treating HSV infection in a patient comprising APC incubated in the presence of (I), in combination with a *carrier"**.

ACTIVITY - Virucide.

MECHANISM OF ACTION - Vaccine.

No biological data is given.

USE - (I) is useful for detecting human immunodeficiency virus (HIV) infection in a patient which involves detecting the presence of antibodies that bind to (I) which is contacted with a biological sample (e.g. whole blood, serum, plasma, saliva, cerebrospinal fluid or urine) obtained from a patient. (I) is also useful for treating HSV infection in a patient which involves incubating peripheral blood cells obtained from the patient in the presence of (I) such that T cells proliferate, and then administering the proliferated T cells to the patient. The T cells are incubated one or more times. Preferably, T cells are separated from the peripheral blood cells obtained from the patient, and incubated in the presence of (I). The obtained T cells are further separated into CD4+ cells or CD8+ T cells from the peripheral blood cells, and are incubated in presence of (I) such that they proliferate. The method further involves separating gamma/delta T lymphocytes from the peripheral blood cells, and proliferating them in the presence of (I). Incubation of the obtained peripheral blood cells further involves cloning one or more T cells that proliferated in the presence of (I). (V) which is capable of binding (I), is useful for detecting HSV infection in a biological sample which involves detecting in the sample, a polypeptide that binds to (V). (VII) and (VIII) are useful for stimulating immune response in a patient. (All claimed). (II) is useful as probes and primers for nucleic acid hybridization. The probes and primers are useful for detecting HSV infection in a patient. (X) is useful for removing HSV infected cells from a biological sample. The treated biological sample is then used for inhibiting the development of HSV infection in a patient.

pp; 157 DwgNo 0/0

14/3,AB/12 (Item 12 from file: 351)
DIALOG(R)File 351:Derwent WPI

014301512

WPI Acc No: 2002-122216/200216
XRAM Acc No: C02-037458
New regulatable, catalytically active nucleic acids (RCANA), useful in gene therapy (particularly for regulating gene expression), or in assays for detecting the presence of ligands or activation of an effector of RCANA
Patent Assignee: UNIV TEXAS SYSTEM (TEXA)
Inventor: COX J C; DAVIDSON E; ELLINGTON A D; HESSELBERTH J; MARSHALL K; REIDEL T; ROBERTSON M; SOOTER L
Number of Countries: 094 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200196559	A2	20011220	WO 2001US19302	A	20010614	200216	B
AU 200168481	A	20011224	AU 200168481	A	20010614	200227	

Priority Applications (No Type Date): US 2000212097 P 20000615
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200196559	A2	E	126	C12N-015/11	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200168481	A		C12N-015/11	Based on patent WO 200196559

Abstract (Basic): WO 200196559 A2
Abstract (Basic):
NOVELTY - A polynucleotide (I), which is regulated by a peptide, is new, where (I) comprises a regulatable, catalytically active nucleic acid (RCANA) or polynucleotide, where the peptide interacts with (I) to affect its catalytic activity.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a nucleic acid segment comprising a RCANA, selected from a pool of nucleic acids in which at least one of the catalytic residues has been randomized;
(2) a RCANA segment comprising:
(a) an effector domain; and
(b) a nucleic acid catalyst domain in which one or more critical catalytic residues of the nucleic acid catalyst have been randomized; where the kinetic parameters of the catalytic domain are regulated by an effector that interacts with the effector domain;
(3) isolating, making or selecting a RCANA;
(4) detecting a target using a RCANA comprising:
(a) contacting the RCANA with the target; an
(b) measuring the effect of the interaction between the RCANA and the target;
(5) modifying a target using a RCANA comprising:
(a) providing a RCANA capable of target specific modification; and
(b) modifying the target under conditions that cause RCANA-specific activity;
(6) biosensors comprising a solid support and at least one RCANA, where the kinetic parameters of the nucleic acids on a target vary in response to the interaction of an effector molecule with the nucleic acid; where:
(i) the nucleic acid construct is immobilized on the support;

(ii) catalytic targets of the catalytic domain is immobilized on the support; or

(iii) the effector is immobilized on the support;

(7) detecting an effector comprising:

(a) mixing a RCANA, where the kinetic parameters of the nucleic acids on a target vary in response to the interaction of an effector molecule with the nucleic acid with the catalytic target of the nucleic acid and effectors;

(b) isolating the RCANA that have reacted with their catalytic targets; and

(c) detecting the RCANA that have reacted with their catalytic targets;

(8) detecting a RCANA comprising:

(a) isolating a RCANA;

(b) creating a construct in which the nucleic acid is in a position to regulate the expression of a *reporter"** gene;

(c) introducing the construct into a host cell; and

(d) measuring the catalytic activity of the nucleic acid upon exposure of the host cell to an effector;

(9) vectors comprising:

(a) a RCANA, where the peptide molecule interacts with the polynucleotide to affect its catalytic activity; or

(b) a RCANA generated by the modification of a catalytic residue;

(10) a device for automatically selecting an aptazyme;

(11) an automated method for selecting aptamer oligonucleotides;

(12) a substrate that produces a signal when an aptazyme reaction occurs comprising a solid support, and at least one aptazyme construct having a regulatable aptamer oligonucleotide sequence with a regulatory domain, where the kinetic parameters of the aptazyme on a target gene vary in response to the interaction of an allosteric effector molecule with the regulatory domain, and where the aptazyme construct is covalently immobilized on the support;

(13) detecting an aptazyme reaction comprising:

(a) providing a substrate comprising a solid support and an aptazyme construct or a heterogenous mixture of aptazyme constructs covalently immobilized on the support;

(b) providing an analyte;

(c) providing a substrate tagged to be detectable;

(d) exposing the substrate and an analyte to the immobilized aptazyme, where the substrate is bound to the immobilized aptazyme upon activation of the aptazyme reaction by the analyte to produce a signal;

(e) washing unbound substrate off of the substrate; and

(f) detecting the signal from the bound substrate; and

(14) modulating the expression of a nucleic acid comprising:

(a) providing a RCANA; and

(b) contacting the polynucleotide with the peptide, thereby modulating expression of a nucleic acid.

ACTIVITY - None given.

MECHANISM OF ACTION - Gene therapy.

USE - The RCANA are useful for regulating gene expression. It is also useful in assays for detecting the presence of ligands or activation of an effector of RCANA. The nucleic acid is particularly useful in gene therapy.

pp; 126 DwgNo 0/31

14/3,AB/13 (Item 13 from file: 351)

DIALOG(R)File 351:Derwent WPI

014127417
WPI Acc No: 2001-611627/200170
XRAM Acc No: C01-182814
XRPX Acc No: N01-456526
New colon tumor proteins and related nucleic acid, useful for treatment, prevention, diagnosis and monitoring of cancer
Patent Assignee: CORIXA CORP (CORI-N); KING G E (KING-I); MEAGHER M J (MEAG-I); XU J (XUJJ-I)
Inventor: KING G E; MEAGHER M J; XU J
Number of Countries: 095 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200173027	A2	20011004	WO 2001US9246	A	20010322	200170 B
US 20010055596	A1	20011227	US 2000191597	A	20000324	200206
			US 2000202024	A	20000504	
			US 2000202189	A	20000505	
			US 2001815343	A	20010322	
AU 200152945	A	20011008	AU 200152945	A	20010322	200208

Priority Applications (No Type Date): US 2000202189 P 20000505; US 2000191597 P 20000324; US 2000202024 P 20000504; US 2001815343 A 20010322
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200173027	A2	E	299	C12N-015/12	
	Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW				
	Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW				
US 20010055596	A1			A61K-039/00	Provisional application US 2000191597
					Provisional application US 2000202024
					Provisional application US 2000202189
AU 200152945	A			C12N-015/12	Based on patent WO 200173027

Abstract (Basic): WO 200173027 A2
Abstract (Basic):

NOVELTY - Isolated polypeptide (I), comprising at least an immunogenic part of a colon tumor protein (CTP) or its variant, is new. CTP is encoded by one of 1556 87-1072 nucleotide sequences (II), all fully defined in the specification, sequences that hybridize to them under moderately strong conditions, or the complements of them.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) isolated polynucleotides (IIa) encoding at least 15 amino acids of a CTP (or its variants with one or more substitutions, deletions, additions and/or insertions that do not significantly reduce reaction with antigen-specific antisera), and their complements;

(2) a nucleic acid comprising (II);

(3) expression vectors containing (II) or (IIa);

(4) host cells transformed or transfected with the vector of (3);

(5) isolated antibody (Ab), or its antigen-binding fragment, that binds specifically to CTP;

fusion protein (FP) that includes (I);

(6) isolated polynucleotides (IIb) that encode FP;
(7) pharmaceutical composition containing a *carrier"** and at least one of (I), (IIa), Ab, FP or (IIb);
(8) vaccine containing an immunostimulant and at least one of (I), (IIa), Ab, FP, (IIb) or antigen-presenting cells (APC) that express (I);
(9) pharmaceutical composition containing an APC that expresses (I) and a *carrier"** or excipient;
(10) removing tumor cells from a sample by treating with T cells that react specifically with CTP;
(11) stimulating and/or expanding CTP-specific T cells by treatment with (I), (II) or APC that express (I);
(12) isolated T cell population produced by the method of (10);
(13) diagnosis and monitoring of cancer by treating samples with CTP-binding agents and comparing the amount of CTP that binds with a predetermined cut-off value, and optionally repeating the procedure at later times;
(14) diagnosis and monitoring of cancer by treating samples with CTP-binding agents and measuring the amount of (II) in a hybridization assay;
(15) diagnostic kit containing Ab and a detectable reagent that includes a *reporter"** group;
(16) oligonucleotides (ON), containing 10-40 contiguous nucleotides, that hybridize under moderately strong conditions to (II); and
(17) diagnostic kit containing ON and reagents for performing polymerase chain reaction or hybridization assay.
ACTIVITY - Cytostatic.
No biological data is given.
MECHANISM OF ACTION - Vaccine; gene therapy.
USE - Compositions and vaccines that contain (I), nucleic acid (II) encoding (I), specific antibodies (Ab), (I)-containing fusion proteins (FP), nucleic acid encoding FP or antigen-presenting cells that express (I) are used to inhibit development (prevention or treatment) of cancer, especially of the colon. T cells that react specifically with CTP are useful for removing tumor cells from samples (e.g. blood) and for cancer treatment (optionally after stimulation/expansion by treating with (I)). Measuring the level of (I) or (II) in a sample is useful for diagnosis and monitoring of cancers, using standard hybridization, amplification or immunological assays.
pp; 299 DwgNo 0/0

14/3,AB/14 (Item 14 from file: 351)
DIALOG(R)File 351:Derwent WPI

013882879
WPI Acc No: 2001-367092/200138
XRAM Acc No: C01-112474
Screening, sequencing and/or quantitating a nucleic acid of interest by hybridizing the nucleic acid with a set of oligonucleotide probes bound to fluorescently addressable microspheres that are suspended in a fluid array
Patent Assignee: LUMINEX CORP (LUMI-N)
Inventor: CHANDLER M B
Number of Countries: 090 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200114589	A2	20010301	WO 2000US22769	A	20000821	200138	B
AU 200067881	A	20010319	AU 200067881	A	20000821	200139	

Priority Applications (No Type Date): US 99149710 P 19990820
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200114589	A2	E	63	C12Q-001/68	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW

AU 200067881	A		C12Q-001/68	Based on patent WO 200114589

Abstract (Basic): WO 200114589 A2
Abstract (Basic):

NOVELTY - Screening, sequencing and/or quantitating a nucleic acid of interest by hybridizing the nucleic acid with a set of oligonucleotide probes bound to fluorescently addressable microspheres that are suspended in a fluid (e.g. liquid, suspension or gaseous array), is new. The identity of the probe is determined by the fluorescent signature of the *microparticle"**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a collection (C1) comprising subpopulations of *particles"**, where the *particles"** in each subpopulation have characteristics that distinguish the *particles"** of the subpopulations and the collection is further characterized as having about 1000 or more distinct subpopulations of *particles"**;

(2) a fluid array comprising:

(a) C1 which has bound nucleic acid; and

(b) a fluid *carrier"**;

(3) a composition of matter comprising a solid *particle"** including:

(a) bound nucleic acid having a known polynucleotide sequence;

(b) a label comprising a dye that exhibits a distinctive fluorescence signature; and

(c) a substance that, in the absence of an analyte of interest comprising a polynucleotide sequence complementary to the known polynucleotide sequence can quench the fluorescence emission of the dye;

(4) of characterizing (M1) a nucleic acid of interest, comprising:

(a) providing oligomer probes of known or ascertainable sequence, bound to a respective number of subpopulations of *particles"** having characteristics that distinguish the *particles"** of the subpopulations so that the sequence of a probe is identifiable according to the unique characteristic of the particular subpopulation of *particles"**;

(b) hybridizing the oligomer probes with the nucleic acid of interest to obtain complementary complexes; and

(c) determining the sequence of the nucleic acid of interest in the complementary complexes by referring to the unique characteristic associated with each subpopulation of *particles"** carrying the probe of known or ascertainable sequence;

(5) quantitating an analyte of interest in a sample comprising:

(a) contacting the sample with a detectable probe bound to a

fluorescently addressable *particle"**; and
(b) measuring the quantity of the analyte by comparing to a standard curve, where the standard curve comprises values from two known quantities of a reference analyte;
(6) an array of nucleic acid probes where each of the probes is bound to a discrete fluorescently addressable set of *microparticles"** , each set is positioned in a predetermined well of a microtiter plate;

(7) a *library"** of oligonucleotide probes of known sequence in which each discrete probe is bound to a respective fluorescent *microparticle"** stained with fluorescent dyes and each dye has the potential of having eight different levels of fluorescence intensity;
(8) a device for identifying an analyte of interest among different analytes in a sample, comprising a fluorescently addressable *microparticle"** having on its surface a bound probe of known sequence labeled with a fluorescent *reporter"** dye, to which the analyte of interest binds in complementary fashion so that the fluorescent *reporter"** dye on the binding probe undergoes a change in fluorescence output indicating the presence of the analyte in the sample and the analyte is identified according to the fluorescent signature of the *microparticle"**;
(9) constructing (M2) a *library"** of oligomer probes of known sequence, comprising:
(a) coupling each of the four bases, A, C, G, and T, to four respective sets of fluorescently distinguishable *microparticles"**;
(b) stacking by means of nucleotide synthesis chemistry to the *microparticle"**-coupled base the next base selected from A, C, G or T;
(c) sorting *microparticles"** according to the formed sequence; and
(d) repeating the nucleotide synthesis and sorting steps (b) and (c) until the desired sequence of the oligomer probe is obtained;
(10) constructing a *library"** of oligomer probes of known sequence, comprising:
(a) synthesizing by nucleotide synthesis chemistry N number of sets of oligomer probes of desired sequence; and
(b) coupling an oligomer probe from one of the N number of sets of oligomer probes to a respective set of fluorescently distinct *microparticles"** labeled with fluorescent dyes having eight different levels of fluorescence intensity;
(11) an array (A1) of nucleic acid probes comprising fluorescently addressable *microparticles"**, each stained with fluorescent dyes and carrying a distinct nucleic acid probe, where the *microparticles"** are arrayed in a two-dimensional pattern over a plane of a microtiter plate;
(12) a liquid array comprising a mixture of sets of fluorescently addressable microspheres in a liquid; and
(13) an enzymatic process for analyzing a nucleic acid sequence present in a sample of interest, comprising:
(a) providing an array of fluorescently addressable *microparticles"** stained with distinct fluorescent dyes;
(b) hybridizing the nucleic acid in the sample of interest with the array; and
(c) analyzing the obtained hybrid by a primer extension enzymatic process.
USE - The method is useful for determining a genetic distance between the nucleic acid of interest and a reference sample. It is also useful for analyzing a nucleic acid of interest comprising at least one

mutation or a set of mutations linked to a clinical condition or a predisposition to the clinical condition, where the clinical is selected from hereditary diseases, neural diseases, muscle and bone diseases, malignant diseases, infectious diseases, metabolic diseases, or their combinations.

The arrays are useful in methods for carrying out sequencing by hybridization, for analyzing gene expression by hybridization of gene-specific mRNA or cDNA to an array of complementary probes, and for quantitating copies of nucleic acid sequences of interest by comparing to a known quantity of a reference material. The array is also useful for screening molecules that bind to array bound nucleic acids, where the molecules have various types of biological activities comprising hormonal, neurotransmitter, metabolic, genetic, pharmacologic, immunologic, pathologic, toxic, and anti-mitotic activities (all claimed).

ADVANTAGE - The methods do not suffer from the inherent limitations imposed by the two dimensional confinements of the gene chip technologies. The method also allows the resolution of up to 1000000 or more unique sets of *particles"**, thus permitting the simultaneous detection of a corresponding number of probes bound to it.

The method is well suited to a multiplexing analysis format and is easily adapted to an automated procedure. The expenses and limitations associated with prior gene chip manufacturing and/or testing procedures are avoided.

pp; 63 DwgNo 0/1

14/3,AB/15 (Item 15 from file: 351)
DIALOG(R)File 351:Derwent WPI

013751059
WPI Acc No: 2001-235288/200124
XRAM Acc No: C01-070625
XRPX Acc No: N01-168193

Assaying *libraries"** of test compounds as ligands and/or substrates of transport proteins, where compounds identified can be linked to pharmaceutical agents therefore facilitating uptake of these agents by a patient

Patent Assignee: XENOPORT INC (XENO-N)
Inventor: BARRETT R W; CHERNOV-ROGAN T; CUNDY K C; DOWER W J; GALLOP M
Number of Countries: 095 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200120331	A1	20010322	WO 2000US25439	A	20000914	200124	B
AU 200077034	A	20010417	AU 200077034	A	20000914	200140	
EP 1212619	A1	20020612	EP 2000966735	A	20000914	200239	
			WO 2000US25439	A	20000914		

Priority Applications (No Type Date): US 99154071 P 19990914
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200120331	A1	E	139	G01N-033/566	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR

IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW
AU 200077034 A G01N-033/566 Based on patent WO 200120331
EP 1212619 A1 E G01N-033/566 Based on patent WO 200120331
Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI

Abstract (Basic): WO 200120331 A1
Abstract (Basic):

NOVELTY - A variety of methods for assaying *libraries"** of test compounds as ligands and/or substrates of transport proteins, including both *carrier"**-type and receptor-type transport proteins, are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are provided for the following:

(1) a method (M1) of screening for a *carrier"**-type transport protein or a receptor-type transport protein and/or its ligand, comprising:

(a) providing a *library"** comprising different complexes, each complex comprising a compound and a *reporter"**, the compound varying between different complexes;

(b) providing a population of cells, one or more of which expresses one or more *carrier"**-type transport proteins;

(c) contacting the population of cells with a complexes from the *library"**; and

(d) detecting a signal from the *reporter"** of a complex that is bound to a cell or internalized within a cell, the signal providing an indication that a complex whose *reporter"** generated the signal comprises a compound that is a ligand for a *carrier"**-type transport protein;

(2) methods (M2) of screening for a *carrier"**-type transport protein and/or its substrate;

(3) a method (M3) of screening for a substrate of a transport protein, comprising:

(a) introducing into a body compartment of an animal a population of complexes, each complex comprising a support, a test compound, and a *reporter"**, the test compound varying between complexes; and

(b) recovering complexes by means of their *reporter"** from a tissue or fluid of the animal after transport of at least some of the complexes through cells lining the body compartment; and

(4) a pharmaceutical composition comprising a *nanoparticle"**, a drug within or linked to the *nanoparticle"** and a ligand linked to or within the *nanoparticle"**, the ligand being effective to promote cellular uptake and/or transport of the *particle"** by receptor-type transport proteins.

ACTIVITY - None given.

No biological data given.

MECHANISM OF ACTION - None given.

No biological data given.

USE - The methods are used for screening individual or test complexes for activity as ligands for various transport proteins. Compounds identified by the methods can be linked to pharmaceutical agents therefore facilitating uptake of these agents by a patient, for e.g. a substrate for an intestinal epithelial cell transporter can be linked to a pharmaceutical agent via a linker that is either enzymatically and/or chemically cleavable or is non-cleavable.

ADVANTAGE - The methods are amenable to high throughput screening formats and can be used to screen large *libraries"** of complexes.

pp; 139 DwgNo 0/30

14/3,AB/16 (Item 16 from file: 351)
DIALOG(R)File 351:Derwent WPI

013523193
WPI Acc No: 2001-007399/200101
XRAM Acc No: C01-001898
XRPX Acc No: N01-005314
A seed-specific promoter from Arabidopsis, useful for controlling gene expression and activating recombination systems, active from an early stage of embyro development
Patent Assignee: RHOBIO (RHOB-N); RHONE-POULENC AGROCHIMIE (RHON)
Inventor: HSIEH T; TERRY L T; THOMAS T L
Number of Countries: 093 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200068388	A1	20001116	WO 2000EP4879	A	20000505	200101	B
AU 200049255	A	20001121	AU 200049255	A	20000505	200112	
US 6342657	B1	20020129	US 99306060	A	19990506	200210	
EP 1177300	A1	20020206	EP 2000931269	A	20000505	200218	
			WO 2000EP4879	A	20000505		

Priority Applications (No Type Date): US 99306060 A 19990506
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200068388	A1	E	70	C12N-015/29	
	Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW				
	Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW				
AU 200049255	A			C12N-015/29	Based on patent WO 200068388
US 6342657	B1			C12N-005/04	
EP 1177300	A1	E		C12N-015/29	Based on patent WO 200068388
	Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI				

Abstract (Basic): WO 200068388 A1
Abstract (Basic):

NOVELTY - A promoter (P) that directs seed-specific expression beginning in the early embryo and hybridizes under stringent conditions to the KNAT411 promoter (which comprises a defined 1697 base pair sequence (1) given in the specification), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(a) plant transformation vectors containing (P);

(b) plant cells containing (P), as a heterologous sequence, or the vector of (a);

(c) a plant or its progeny regenerated from the cells of (b);

(d) an expression cassette (EC1) comprising (P) linked to at least one nucleic acid that is a heterologous gene or encodes a sequence complementary to a native plant gene;

(e) expression cassette (EC2) containing (P) linked to a Cre, FLP, R or Gin recombinase gene;

(f) expression vectors containing EC1 or EC2;

(g) cells containing EC1 or EC2;

(h) transgenic plants containing EC1 or EC2, and their progeny or seeds; and

(i) plants regenerated from cells of (g), or their progeny or seeds.

USE - (P) is used in plant-transformation vectors to direct seed-specific expression of genes or sequences complementary to an endogenous plant gene and to activate a site-specific recombination system in the early embryo, resulting in a recombination event that is fixed in the germline of the plant. Particularly (1) is used to increase or decrease (by antisense or co-suppression techniques) levels of genes involved in fatty acid synthesis or lipid metabolism and (2) is used to excise or invert anonymous genes involved in embryo or seed development, or those of unknown function, for which no stable mutations are available.

ADVANTAGE - (P) are active at a much earlier stage in embryo development than known seed-specific promoters.

pp; 70 DwgNo 0/8

14/3,AB/17 (Item 17 from file: 351)
DIALOG(R)File 351:Derwent WPI

013270765
WPI Acc No: 2000-442671/200038
Related WPI Acc No: 2001-441847
XRAM Acc No: C00-134755
XRPX Acc No: N00-330235

New colon tumor polypeptides used to inhibit the development of cancer, especially colon cancer, and for diagnosing and monitoring the progression of the cancer

Patent Assignee: CORIXA CORP (CORI-N); CLAPPER J D (CLAP-I); MEAGHER M J (MEAG-I); STOLK J A (STOL-I); WANG A (WANG-I)

Inventor: BENSON D R; LODES M J; MEAGHER M J; SECRIST H; STOLK J; WANG T; XU J; YUQIU J; CLAPPER J D; JIANG Y; KING G E; SMITH C L; STOLK J A; WANG A

Number of Countries: 091 Number of Patents: 006

Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200037643	A2	20000629	WO 99US30909	A	19991223	200038	B
AU 200023879	A	20000712	AU 200023879	A	19991223	200048	
US 6284241	B1	20010904	US 98221298	A	19981223	200154	
EP 1144632	A2	20011017	EP 99967625	A	19991223	200169	
			WO 99US30909	A	19991223		
US 20020076414	A1	20020620	US 98221298	A	19981223	200244	
			US 99347496	A	19990702		
			US 99401064	A	19990922		
			US 99454150	A	19991202		
			US 99476296	A	19991230		
			US 2000480321	A	20000110		
			US 2000504629	A	20000215		
			US 2000519444	A	20000306		
			US 2000444252	A	20000410		
			US 2000575251	A	20000519		
			US 2000609448	A	20000629		
			US 2000649811	A	20000828		
			US 2001833263	A	20010410		
			US 2001922217	A	20010803		

US 20020110547	A1	20020815	US 98221298	A	19981223	200256	
			US 99347496	A	19990702		
			US 99401064	A	19990922		
			US 99454150	A	19991202		
			WO 99US30909	A	19991223		
			US 99476296	A	19991230		
			US 2000480321	A	20000110		
			US 2000504629	A	20000215		
			US 2000519444	A	20000306		
			US 2000444252	A	20000410		
			US 2000575251	A	20000519		
			US 2000609448	A	20000629		
			US 2000649811	A	20000828		
			US 2001833263	A	20010410		

Priority Applications (No Type Date): US 99454150 A 19991202; US 98221298 A 19981223; US 99347496 A 19990702; US 99401064 A 19990922; US 99444242 A 19991119

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200037643	A2	E	227	C12N-015/12	
Designated States (National): AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
AU 200023879	A			C12N-015/12	Based on patent WO 200037643
US 6284241	B1			C12N-015/00	
EP 1144632	A2	E		C12N-015/12	Based on patent WO 200037643
Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
US 20020076414	A1			A61K-039/00	CIP of application US 98221298
					CIP of application US 99347496
					CIP of application US 99401064
					CIP of application US 99454150
					CIP of application US 99476296
					CIP of application US 2000480321
					CIP of application US 2000504629
					CIP of application US 2000519444
					CIP of application US 2000444252
					CIP of application US 2000575251
					CIP of application US 2000609448
					CIP of application US 2000649811
					CIP of application US 2001833263
US 20020110547	A1			A61K-038/43	CIP of application US 98221298
					CIP of application US 99347496
					CIP of application US 99401064
					CIP of application US 99454150
					CIP of application WO 99US30909
					CIP of application US 99476296
					CIP of application US 2000480321
					CIP of application US 2000504629
					CIP of application US 2000519444
					CIP of application US 2000444252
					CIP of application US 2000575251
					CIP of application US 2000609448
					CIP of application US 2000649811

Searcher : Shears 308-4994

Abstract (Basic): WO 200037643 A2
Abstract (Basic):

NOVELTY - An isolated polypeptide, (I) comprising at least an immunogenic portion of a colon tumor protein, and having an amino acid sequence encoded by one of 222 nucleic acid sequences, all fully defined in the specification, or sequences which hybridizes to them, or their complements, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an isolated polypeptide comprising a 683, 168, 168, 200, 201, 135, 135, or 167 residue amino acid sequence, all fully defined in the specification;

(2) an isolated polynucleotide (II) encoding at least 15 amino acids of a colon tumor protein, or variants of them, where the amino acid sequence is encoded by one of 222 nucleic acid sequences, all fully defined in the specification;

(3) an isolated polynucleotide (III) comprising, or hybridizing to one of the 222 nucleic acid sequences;

(4) an isolated polynucleotide (IV) complementary to (I) or (II);

(5) an expression vector (V) comprising (I), (II), or (III);

(6) a host cell transformed or transfected with (V);

(7) an antibody (VI), or fragment specific for (I);

(8) a fusion protein (VII) comprising at least one (I);

(9) an isolated polynucleotide (VIII) encoding a fusion protein of (8);

(10) a pharmaceutical composition comprising a *carrier"** and (I), (II), (VI), (VII), (VIII), or an antigen presenting cell expressing (I);

(11) a vaccine comprising an immunostimulant and (I), (II), (VI), (VII), or (VIII);

(12) removing tumor cells from a sample, comprising contacting the sample with T-cells specific for (I) encoded by one of 478 nucleic acid sequences, all fully defined in the specification, or their complements;

(13) stimulating and/or expanding T-cells specific for a colon tumor protein, comprising contacting T-cells with at least one of (I), (II), a polypeptide encoded by one of the 478 nucleic acid sequences, a polynucleotide encoding them, and an antigen presenting cell expressing one of the polypeptides;

(14) an isolated T-cell population, comprising T-cells produced by the method of (13);

(15) an oligonucleotide, comprising 10-40 contiguous nucleotides that hybridizes to (II) under moderately stringent conditions;

(16) a diagnostic kit, comprising one or more (VI), and a detection reagent, comprising a *reporter"** group; and

(17) a diagnostic kit, comprising an oligonucleotide of (15), and a diagnostic reagent for use in polymerase chain reaction, or hybridization assay.

ACTIVITY - Cytostatic.

MECHANISM OF ACTION - Vaccine targeting colon tumor antigens.

USE - The pharmaceutical compositions, vaccines, and antigen presenting cells (APC), preferably dendritic cells, expressing a polypeptide encoded by one of 478 nucleic acid sequences, all fully defined in the specification, are used to inhibit the development of cancer, especially colon cancer (claimed). T-cells specific for the polypeptide expressed by the APC, are used to remove tumor cells from biological samples, especially blood, or fractions of it, the sample

can then be used to inhibit cancer development (claimed). The isolated T-cells specific for (I) can also be used to inhibit cancer development (claimed). Cancer development may also be inhibited by incubating CD4+ and/or CD8+ T cells of a patient with (I), (II), the polypeptide expressed by the APC, or the APC itself, to proliferate the T cells, optionally cloning the cells, and administering them to the patient (claimed). The presence or absence of cancer, especially colon cancer in a patient may be determined by contacting a sample with a binding agent, preferably a monoclonal antibody specific for a colon tumor protein expressed by the APC, or its complement, and comparing detected binding to a predetermined cut off value (claimed). The presence or absence of cancer, may alternatively be monitored by contacting a sample with an oligonucleotide which hybridizes to one of the 478 nucleic acid sequences, or their complements, and comparing hybridization levels with a predetermined cutoff value (claimed). The amount of hybridization is determined by polymerase chain reaction, or hybridization assay (claimed). The progression of a cancer can be monitored by repeating the processes at time intervals, and comparing the current result to previous results (claimed).

ADVANTAGE - None given.

pp; 227 DwgNo 0/0

14/3,AB/18 (Item 18 from file: 351)
DIALOG(R)File 351:Derwent WPI

012988822
WPI Acc No: 2000-160675/200014
Related WPI Acc No: 1998-609891; 2002-062250
XRAM Acc No: C00-050162
XRPX Acc No: N00-119888

New compounds and methods for the diagnosis of Ehrlichia infection, particularly Human granulocytic ehrilichiosis

Patent Assignee: CORIXA CORP (CORI-N); HOUGHTON R L (HOUG-I); LODES M J (LODE-I); MCNEILL P D (MCNE-I); REED S G (REED-I)
Inventor: HOUGHTON R L; LODES M J; MCNEILL P D; REED S G
Number of Countries: 085 Number of Patents: 006
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200000615	A2	20000106	WO 99US14793	A	19990629	200014	B
AU 9948474	A	20000117	AU 9948474	A	19990629	200026	
US 6277381	B1	20010821	US 97821324	A	19970321	200150	
			US 97975762	A	19971120		
			US 98106582	A	19980629		
			US 98159469	A	19980923		
			US 99295028	A	19990420		
US 6306402	B1	20011023	US 97821324	A	19970321	200165	
			US 97975762	A	19971120		
			US 98106582	A	19980629		
EP 1144639	A2	20011017	EP 99932087	A	19990629	200169	
			WO 99US14793	A	19990629		
US 20020064535	A1	20020530	US 97821324	A	19970321	200240	
			US 97975762	A	19971120		
			US 98106582	A	19980629		
			US 98159469	A	19980923		

Priority Applications (No Type Date): US 99295028 A 19990420; US 98106582 A

19980629; US 98159469 A 19980923; US 97821324 A 19970321; US 97975762 A 19971120

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200000615	A2	E	108	C12N-015/31	
Designated States (National): AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZA ZW					
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
AU 9948474	A			C12N-015/31	Based on patent WO 200000615
US 6277381	B1			A61K-039/02	CIP of application US 97821324 CIP of application US 97975762 CIP of application US 98106582 CIP of application US 98159469
US 6306402	B1			A61K-039/02	CIP of application US 97821324 CIP of application US 97975762
EP 1144639	A2	E		C12N-015/31	Based on patent WO 200000615
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
US 20020064535	A1			A61K-039/02	CIP of application US 97821324 CIP of application US 97975762 Cont of application US 98106582 CIP of patent US 6207169 CIP of patent US 6231869 Cont of patent US 6306402

Abstract (Basic): WO 200000615 A2

Abstract (Basic):

NOVELTY - A polypeptide (P) comprising an immunogenic portion of an Ehrlichiaantigen or its variant that is encoded by one of 18 DNA sequences of 201-7091 base pairs (bp) (I)-(XVIII) (all sequences fully defined in the specification), their complements and DNA sequences that hybridize to sequences (I)-(XVIII), are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) An antigenic epitope (E) of an Ehrlichia antigen comprising an amino acid sequence of (XIX) or (XX) consisting of 41 and 125 amino acids (aa) respectively (both sequences fully defined in the specification);

(2) A polypeptide (P') comprising at least one of (E);

(3) A DNA molecule (N) comprising a nucleotide sequence encoding (P) or (P');

(4) A recombinant expression vector (V) comprising (N);

(5) A host cell (H) transformed with (N);

(6) A fusion protein (F) comprising either at least one of (P) or (P') and/or at least one of (E) or a 376 aa sequence (XXI) fully defined in the specification;

(7) Method (A) of detecting Ehrlichia infection, Lyme disease and Babesia microtiinfection in a patient comprising:

(a) contacting a biological sample with at least one of (E), (P), (P') or (F) and a Lyme disease antigen and a B.microti antigen; and

(b) detecting the presence of antibodies that bind to (E), (P), (P') or (F) or the Lyme disease antigen or the B.microti antigen in the sample;

(8) Method (B) of detecting Ehrlichia infection, Lyme disease and B.microtiinfection in a patient comprising:

(a) contacting a biological sample with a specific binding agent to at least one of (E), (P), (P') or (F) or a Lyme disease antigen and a B.microti antigen; and

(b) detecting a polypeptide that binds to the binding agent, thereby detecting Ehrlichiainfection;

(9) Method (C) of detecting Ehrlichia infection in a biological sample comprising:

(a) contacting the sample with one or more probe oligonucleotides (or at least two primer oligonucleotides in a PCR reaction) where at least one is specific for (N); and

(b) detecting in the sample a DNA sequence that hybridizes to (or amplifies in the presence of) the oligonucleotide primers, thereby detecting Ehrlichia infection;

(10) A diagnostic kit (K) comprising:

(a) at least one of (P), (P'), (E) or (F); and

(b) a detection agent;

(11) A diagnostic kit (K') comprising at least two oligonucleotide primers or one oligonucleotide probe whereby at least one is specific for (N);

(12) A monoclonal antibody or polyclonal antibody that binds to (P), (P') or (E); and

(13) Vaccines comprising at least one of (P), (P'), (N) or (E) and a non-specific immune enhancer such as an adjuvant.

USE - (P), (P'), (N), (F) and/or (E) are useful for the detection and treatment of Ehrlichiainfection. (P), (P'), (F) and/or (E) can also be used to detect Lyme disease and B.microti infection. In particular, (P') can be used for the serodiagnosis and treatment of human granulocytic ehrlichiosis (HGE). (P) or (P'), (N) and (E) can be contained within a pharmaceutical composition together with a physiologically acceptable *carrier"**. These compositions can be used in the manufacture of a medicament for inducing protective immunity in a patient. The new vaccines are also used for inducing protective immunity in a patient.

ADVANTAGE - The accurate and early diagnosis of Ehrlichia infection is critical but current methods are time-consuming, labor-intensive and expensive. The new compositons and methods overcome these problems.

pp; 108 DwgNo 0/2

14/3,AB/19 (Item 19 from file: 351)
DIALOG(R)File 351:Derwent WPI

012672944
WPI Acc No: 1999-479051/199940
Related WPI Acc No: 2000-062456
XRAM Acc No: C99-140949
XRPX Acc No: N99-356654
Differentiation-associated proteins and related polynucleotides, useful for vaccine and pharmaceuticals to inhibit cell growth
Patent Assignee: GENQUEST INC (GENQ-N); MOTOROLA INC (MOTI)
Inventor: STALO W J; FISHER P B; HUANG F
Number of Countries: 083 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 9937774	A2	19990729	WO 99US1549	A	19990125	199940	B
AU 9924697	A	19990809	AU 9924697	A	19990125	200001	
US 6266530	B1	20010724	US 9887167	A	19980529	200146	

Priority Applications (No Type Date): US 9887167 A 19980529; US 9873298 P 19980126; US 9874441 P 19980211; US 9877804 P 19980312; US 9879326 P 19980325; US 9883195 P 19980428; US 9885609 P 19980515; US 9886829 P 19980526

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 9937774	A2	E	142	C12N-015/12	

Designated States (National): AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW

Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

AU 9924697	A	C12N-015/12	Based on patent WO 9937774	
US 6266530	B1	H04Q-007/20		

Abstract (Basic): WO 9937774 A2

Abstract (Basic):

NOVELTY - Polypeptides associated with terminal differentiation and growth arrest are new.

DETAILED DESCRIPTION - An isolated polypeptide (P) comprises at least a portion of a differentiation-associated protein (DAP) or a variant, where:

(a) the DAP comprises a sequence encoded by one of 70 polynucleotides (ranging from 97 to 903 bp in length, given in the specification); and

(b) the portion retains at least one immunological and/or biological activity characteristic of the DAP.

INDEPENDENT CLAIMS are also included for the following:

(1) an isolated polynucleotide (I) encoding (P);

(2) an antisense polynucleotide comprising a sequence complementary to (I);

(3) an expression vector comprising (I);

(4) a host cell transformed or transfected with an expression vector as in (3);

(5) pharmaceutical composition or vaccine comprising (P) and a physiologically acceptable *carrier"** or immune response enhancer, respectively;

(6) a vaccine comprising (P) and an immune response enhancer;

(7) a monoclonal antibody or antigen-binding fragment that specifically binds to (P);

(8) recombinant production of (P) comprises culturing the host cell of (4);

(9) a method for identifying a compound/agent that modulates cell growth and/or differentiation;

(10) a polynucleotide comprising an endogenous promoter or regulatory element of a DAP as above;

(11) a polynucleotide comprising a *reporter"** gene under the control of an endogenous promoter or regulatory element of a DAP as above;

(12) a cell transformed or transfected with a polynucleotide as in (10) or (11); and

(13) a method for identifying an agent that modulates the expression of a DAP.

(14) a method for inhibiting the development of a cancer in a patient, comprises administering (I) to a patient, under conditions such that the polynucleotide enters a cell of the patient and is

expressed;
(15) a method for determining whether a tumor in a patient is malignant, comprising determining the level of (P) or detecting (I) in a tumor sample obtained from a patient, and therefore determining whether the tumor is malignant;
(16) a method for monitoring the progression of a cancer in a patient, comprising:
(a) detecting, in a biological sample obtained from a patient, an amount of (P) or an amount of an RNA molecule encoding (P) at a first point in time; at a first point in time;
(b) repeating step (a) at a subsequent point in time; and
(c) comparing the amounts of polypeptide or RNA detected in steps (a) and (b), and therefore monitoring the progression of a cancer in the patient;
(17) a diagnostic kit, comprising:
(a) a monoclonal antibody or its fragment; and
(b) a second monoclonal antibody or fragment thereof that binds to:
(i) a monoclonal antibody recited in step (a); or
(ii) (P); where the second monoclonal antibody is conjugated to a *reporter"** group;
(18) a method for identifying a compound that modulates cell growth and/or differentiation
(19) a method for inhibiting the development of a cancer in a patient, comprising the step of administering to a patient an agent that increases expression of (P), and therefore inhibiting the development of a cancer in the patient.
ACTIVITY - Cytostatic.
MECHANISM OF ACTION - Vaccine; Antibody; DAP Inhibitor.
USE - The DAP, a DAP fragment or a DAP polynucleotide can be used to inhibit the development of cancer including prostate, breast, lung and colorectal cancer, melanoma, astrocytoma or glioblastoma multiforme. Determining the level of a DAP or its coding sequence, with e.g. a monoclonal antibody against a DAP or a DAP gene probe, in a tumor sample can be used to determine whether the tumor is malignant. The progression of cancer can be monitored by measuring DAP expression/activity levels over a period of time. An agent that increases expression of a DAP can also be used to inhibit the development of cancer (all claimed).
pp; 142 DwgNo 0/66

14/3,AB/20 (Item 20 from file: 351)
DIALOG(R)File 351:Derwent WPI

012588765
WPI Acc No: 1999-394872/199933
Related WPI Acc No: 1999-371184; 1999-395229
XRAM Acc No: C99-116022
XRPX Acc No: N99-295161
Identifying interacting molecules by automated interaction mating
Patent Assignee: MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN (PLAC)
Inventor: BRANCROFT D; LEHRACH H; WANKER E; WEDEMEYER N
Number of Countries: 084 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 9928745	A1	19990610	WO 98EP7657	A	19981127	199933	B
AU 9920505	A	19990616	AU 9920505	A	19981127	199945	

EP 1036324	A1	20000920	EP 98965193	A	19981127	200047
			WO 98EP7657	A	19981127	
JP 2002507386	W	20020312	WO 98EP7657	A	19981127	200220
			JP 2000523551	A	19981127	

Priority Applications (No Type Date): EP 97120880 A 19971127; EP 97120867 A 19971127; EP 97120879 A 19971127

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 9928745	A1	E	193	G01N-033/50	

Designated States (National): AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW

Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

AU 9920505	A		G01N-033/50	Based on patent WO 9928745
EP 1036324	A1	E	G01N-033/50	Based on patent WO 9928745

Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI

JP 2002507386	W		177	C12N-015/09	Based on patent WO 9928745

Abstract (Basic): WO 9928745 A1

Abstract (Basic):

NOVELTY - A new method for identifying interacting molecules comprises using host cells which are able to grow on different selective media and a genetic system that activates a readout system.

DETAILED DESCRIPTION - The method (M1) for the identification of at least one member of a pair or complex of interacting molecules from a pool of potentially interacting molecules, comprises:

(a) providing at least one set of host cells, each set containing at least one genetic element comprising a selectable marker, the selectable marker being different between different sets of host cells, the genetic elements each comprising genetic information specifying one of the potentially interacting molecules, the host cells further carrying a readout system that is activated upon the presence of auto-activating molecules;

(b) selecting against host cells expressing a molecule able to auto-activate the readout system by transferring at least one set of host cells or progeny of at least one set of host cells to at least one selective medium which allows growth of the host cells in the presence of the selectable marker different for each set of host cells and which precludes growth of the host cells upon auto-activation of the readout system;

(c) combining in host cells at least two genetic elements, where at least one set of host cells grows on the selective medium specified in (b);

(d) allowing at least one interaction, if any, to occur;

(e) selecting for the interaction by transferring the host cells or progeny of the host cells to a selective medium that allows identification of the host cells upon activation of the readout system;

(f) identifying host cells that contain interacting molecules that activate the readout system on the selective medium;

(g) identifying at least one member of the pair or complex of interacting molecules;

where the host cells are not yeast cells.

INDEPENDENT CLAIMS are also included for the following:

(1) a method for the identification of at least one member of a

pair or complex of interacting molecules from a pool of potentially interacting molecules, comprising:

(i) step (a) as in (M1);

(ii) selecting against host cells expressing a molecule able to auto-activate the readout system by transferring at least one set of host cells or progeny of at least one set of host cells to at least one selective medium which allows growth of the host cells in the presence of the selectable marker different for each set of host cells and visual differentiation between those cells whose readout system has been activated from those host cells whose readout system has not been activated;

(iii) steps (c)-(f) as in (M1);

(iv) identifying at least one member of the pair or complex of interacting molecules;

(2) a method for the identification of at least one member of a pair or complex of interacting molecules from a pool of potentially interacting molecules, comprising:

(i) steps (a)-(f) as in (M1);

(ii) identifying at least one member of the pair or complex of interacting molecules; where the host cells are yeast cells, and at least one of the steps (b), (c), (e) or (f) is effected or assisted by automation using regular grid patterns of host cells;

(3) a kit comprising:

(i) host cells comprising a readout system which allows host cells to be counterselected against auto-activation of the readout system; and

(ii) at least one genetic element comprising a selectable marker, a counterselectable marker and genetic information encoding an activation domain or a DNA binding domain, which activation domain and DNA binding domain are together able to activate the readout system; where the host cells are not yeast cells; and

(4) a kit comprising:

(a) host cells comprising a readout system which allows host cells to be visually differentiated upon activation of the readout system; and

(b) at least one genetic element comprising a selectable marker and genetic information encoding an activation domain or a DNA binding domain, which activation domain and DNA binding domain are together able to activate the readout system.

USE - The methods can be used for identifying interacting molecules such as RNA-RNA, RNA-DNA, RNA-protein, DNA-DNA, DNA-protein, protein-peptide, peptide-peptide or protein-protein interactions (claimed). The method provides for high throughput interaction screens for the reliable identification of interacting molecules, which in turn can lead to the identification of substances inhibiting the interactions. Such inhibitors can find their use in the formulation of a pharmaceutical composition.

ADVANTAGE - The method provides a reliable way for the detection of false positive clones that express fusion proteins which are able to activate the readout system without an interaction with a second molecule.

pp; 193 DwgNo 0/22

14/3,AB/21 (Item 21 from file: 351)
DIALOG(R)File 351:Derwent WPI

012531587
WPI Acc No: 1999-337693/199928
XRAM Acc No: C99-099297
*Carrier"**-*reporter"** *bead"** assemblies used to form a synthetic oligomer *library"** preferably by a combinatorial split-process-recombine procedure
Patent Assignee: UNIV QUEENSLAND (UYQU)
Inventor: BRYANT D E; TRAU M
Number of Countries: 083 Number of Patents: 005
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 9924458	A1	19990520	WO 98AU944	A	19981112	199928	B
AU 9911362	A	19990531	AU 9911362	A	19981112	199941	
EP 1034183	A1	20000913	EP 98954064	A	19981112	200046	
			WO 98AU944	A	19981112		
JP 2001522861	W	20011120	WO 98AU944	A	19981112	200204	
			JP 2000520466	A	19981112		
AU 742678	B	20020110	AU 9911362	A	19981112	200217	

Priority Applications (No Type Date): AU 97328 A 19971112
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 9924458	A1	E	82	C07K-001/10	
Designated States (National): AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW					
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW					
AU 9911362	A			C07K-001/10	Based on patent WO 9924458
EP 1034183	A1	E		C07K-001/10	Based on patent WO 9924458
Designated States (Regional): DE ES FR GB IT					
JP 2001522861	W		80	C07K-001/10	Based on patent WO 9924458
AU 742678	B			C07K-001/10	Previous Publ. patent AU 9911362 Based on patent WO 9924458

Abstract (Basic): WO 9924458 A1
Abstract (Basic):

NOVELTY - A method of forming a synthetic oligomer *library"** comprising a plurality of molecules comprising a multiplicity of different chemical groups is claimed.

DETAILED DESCRIPTION - The method comprises:

(i) attaching a chemical group to a *carrier"** in each of a plurality of reaction vessels;

(ii) attaching a *reporter"** *bead"** to the *carrier"** in a non-covalent manner in each reaction vessel where each *reporter"** *bead"** has a marker associated with it to identify the chemical group attached to the *carrier"** as well as to identify the position in sequence of the chemical group relative to other chemical groups in each molecule;

(iii) combining the *carriers"** from each reaction vessel into a recombination vessel; (iv) splitting the *carriers"** from the recombination vessel into the reaction vessels where steps (i) and (ii) are repeated;

(v) repeating steps (iii) and (iv) until the *library"** is formed where each molecule will have a unique signal associated with it which is dependent on different combinations of markers to facilitate direct identification of the sequence of chemical groups comprising the

molecule.
Step (ii) can be carried out before or at the same time as step.
INDEPENDENT CLAIMS are also included for:
(1) an oligomer *library"** comprising a plurality of different molecules each having a multiplicity of different chemical groups formed by the method;
(2) an oligomer *library"** comprising a plurality of different molecules each attached to a *carrier"** to which are attached *reporter"** *beads"**;
(3) an assembly of a *carrier"** having one or more *reporter"** *beads"** non-covalently attached; and
(4) a method of forming an assembly of a *carrier"** and *reporter"** *beads"**.
USE - The assembly of a *carrier"** and one or more *reporter"** *beads"** may be used to form a synthetic oligomer *library"** preferably by a combinatorial split-process-recombine procedure.
ADVANTAGE - A molecule of interest in the oligomer *library"** may be directly identified or decoded without the requirement of any preliminary step.
pp; 82 DwgNo 0/0

14/3,AB/22 (Item 1 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

13566012 Document Delivery Available: 000174366700018 References: 17
TITLE: Multi-fluorescent silica colloids for encoding large combinatorial *libraries"**
AUTHOR(S): Matthews DC; Grondahl L; Battersby BJ; Trau M (REPRINT)
AUTHOR(S) E-MAIL: trau@chemistry.uq.edu.au
CORPORATE SOURCE: Univ Queensland, Ctr Nanotechnol & Biomat, /Brisbane/Qld 4072/Australia/ (REPRINT); Univ Queensland, Ctr Nanotechnol & Biomat, /Brisbane/Qld 4072/Australia/
PUBLICATION TYPE: JOURNAL
PUBLICATION: AUSTRALIAN JOURNAL OF CHEMISTRY, 2001, V54, N9-10, P649-656
GENUINE ARTICLE#: 530NW
PUBLISHER: C S I R O PUBLISHING, 150 OXFORD ST, PO BOX 1139, COLLINGWOOD, VICTORIA 3066, AUSTRALIA
ISSN: 0004-9425
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Large chemical *libraries"** can be synthesized on solid-support *beads"** by the combinatorial split-and-mix method. A major challenge associated with this type of *library"** synthesis is distinguishing between the *beads"** and their attached compounds. A new method of encoding these solid-support *beads"**, 'colloidal bar-coding', involves attaching fluorescent silica colloids ('*reporters"**') to the *beads"** as they pass through the compound synthesis, thereby creating a fluorescent bar code on each *bead"**. In order to obtain sufficient *reporter"** varieties to bar code extremely large *libraries"**, many of the *reporters"** must contain multiple fluorescent dyes. We describe here the synthesis and spectroscopic analysis of various mono- and multi-fluorescent silica *particles"** for this purpose. It was found that by increasing the amount of a single dye introduced into the *particle"** reaction mixture, mono- fluorescent silica *particles"** of increasing intensities could be prepared. This increase was highly reproducible and was observed for six different fluorescent dyes. Multi-fluorescent silica *particles"**

containing up to six fluorescent dyes were also prepared. The resultant emission intensity of each dye in the multi-fluorescent *particles"** was found to be dependent upon a number of factors; the hydrolysis rate of each silane-dye conjugate, the magnitude of the inherent emission intensity of each dye within the silica matrix, and energy transfer effects between dyes. We show that by varying the relative concentration of each silane-dye conjugate in the synthesis of multi-fluorescent *particles"**, it is possible to change and optimize the resultant emission intensity of each dye to enable viewing in a fluorescence detection instrument.

14/3,AB/23 (Item 2 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12235615 References: 18
TITLE: Encoding combinatorial *libraries"**: A novel application of fluorescent silica colloids
AUTHOR(S): Grondahl L; Battersby BJ; Bryant D; Trau M (REPRINT)
AUTHOR(S) E-MAIL: trau@chemistry.uq.edu.au
CORPORATE SOURCE: Univ Queensland, Dept Chem, /St Lucia/Qld 4072/Australia/ (REPRINT); Univ Queensland, Dept Chem, /St Lucia/Qld 4072/Australia/; Univ Queensland, Dept Math, /St Lucia/Qld 4072/Australia/
PUBLICATION TYPE: JOURNAL
PUBLICATION: LANGMUIR, 2000, V16, N25 (DEC 12), P9709-9715
GENUINE ARTICLE#: 380VM
PUBLISHER: AMER CHEMICAL SOC, 1155 16TH ST, NW, WASHINGTON, DC 20036 USA
ISSN: 0743-7463
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: A major challenge associated with using large chemical *libraries"** synthesized on microscopic solid support *beads"** is the rapid discrimination of individual compounds in these *libraries"**. This challenge can be overcome by encoding the *beads"** with 1 mum silica colloidal *particles"** ("*reporters"**") that contain specific and identifiable combinations of fluorescent byes. The colored bar code generated on support *beads"** during combinatorial *library"** synthesis can be easily, rapidly, and inexpensively decoded through the use of fluorescence microscopy. All *reporters"** are precoated with polyelectrolytes [poly(acrylic acid), PAA, poly(sodium 4-styrenesulfonate PSSS, polyethylenimine, PEI, and/or poly(diallyldimethylammonium chloride), PDADMAC] with the aim of enhancing surface charge, promoting electrostatic attraction to the *bead"**, and facilitating polymer bridging between the *bead"** and *reporter"** for permanent adhesion. As shown in this article, *reporters"** coated with polyelectrolytes clearly outperform uncoated *reporters"** with regard to quantity of attached *reporters"** per *bead"** (54 +/- 23 in 2500 mum(2) area for PEI/PAA coated and 11 +/- 6 for uncoated *reporters"**) and minimization of cross-contamination (1 red *reporter"** in 2500 mum(2) area of green-labeled *bead"** for PEI/PAA coated and 26 +/- 15 red *reporters"** on green-labeled *beads"** for uncoated *reporters"** after 10 days). Examination of various polyelectrolyte systems shows that the magnitude of the xi -potential of polyelectrolyte-coated *reporters"** (-64 mV for PDADMAC/PSSS and -42 mV for PEI/PAA-coated *reporters"**) has no correlation with the number of *reporters"** that adhere to the solid support *beads"** (21 +/- 16 in 2500 mum(2) area for PDADMAC/PSSS and 54 +/- 23 for PEI/PAA-coated *reporters"**). The contribution of polymer bridging to the adhesion has a far greater influence than electrostatic attraction and is demonstrated by modification

of the polyelectrolyte multilayers using gamma irradiation of precoated *reporters"** either in aqueous solution or in polyelectrolyte solution.

14/3,AB/24 (Item 1 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

09831445 Supplier Number: 87015124
Access to government information in a post 9/11 world.
Gordon-Murnane, Laura
Searcher, v10, n6, p50(13)
June, 2002
Language: English Record Type: Fulltext
Document Type: Magazine/Journal; Professional Trade
Word Count: 9490

14/3,AB/25 (Item 2 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

09316390 Supplier Number: 81163609
Product Listings: Laboratory Apparatus & Testing Equipment.
The Journal of Coatings Technology, v73, n922, p175(8)
Nov, 2001
Language: English Record Type: Fulltext
Document Type: Magazine/Journal; Trade
Word Count: 5020

14/3,AB/26 (Item 3 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

09316386 Supplier Number: 81163605
Supplier Listings: Services.
The Journal of Coatings Technology, v73, n922, p106(12)
Nov, 2001
Language: English Record Type: Fulltext
Document Type: Magazine/Journal; Trade
Word Count: 8358

14/3,AB/27 (Item 4 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

06821944 Supplier Number: 57632127
EUROPEAN PATENT DISCLOSURES PRIVATE.
BIOWORLD Today, vVol. 10, nNo. 221, pNA
Nov 18, 1999
Language: English Record Type: Fulltext
Document Type: Magazine/Journal; Trade
Word Count: 2074

14/3,AB/28 (Item 5 from file: 16)

DIALOG(R)File 16:Gale Group PROMT(R)

05996748 Supplier Number: 53375070
TB Vaccines "Rehabilitating Mycobacterium tuberculosis: From Pathogenesis to Vaccine Development.".
Tuberculosis & Airborne Disease Weekly, pNA
Dec 7, 1998
Language: English Record Type: Fulltext
Document Type: Newsletter; Trade
Word Count: 308

14/3,AB/29 (Item 6 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

03461311 Supplier Number: 44830547
The Internet goes visual on the Web
Modern Healthcare, p50
July 11, 1994
Language: English Record Type: Fulltext
Document Type: Magazine/Journal; Professional
Word Count: 1246

14/3,AB/30 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

137289890 CA: 137(20)289890v PATENT
DART conjugates of proteins and nucleic acids for use as analytical and therapeutic tools
INVENTOR(AUTHOR): Roberts, Radclyffe L.; De Figueiredo, Paul
LOCATION: USA
ASSIGNEE: University of Washington
PATENT: PCT International ; WO 200279393 A2 DATE: 20021010
APPLICATION: WO 2002US10566 (20020402) *US PV281133 (20010402) *US PV281342 (20010403)
PAGES: 205 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-000/A
DESIGNATED COUNTRIES: AE; AG; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; BZ; CA; CH; CN; CO; CR; CU; CZ; DE; DK; DM; DZ; EC; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MA; MD; MG; MK; MN; MW; MX; MZ; NO; NZ; OM; PH; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TN; TR; TT; TZ; UA; UG; US; UZ; VN; YU; ZA; ZM; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW ; MZ; SD; SL; SZ; TZ; UG; ZM; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; TR; BF; BJ; CF; CG; CI; CM; GA; GN; GQ; GW; ML; MR; NE; SN; TD; TG

14/3,AB/31 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

136320313 CA: 136(21)320313q PATENT
High throughput or capillary-based screening of libraries of compounds for biological activities

INVENTOR(AUTHOR): Short, Jay M.; Keller, Martin; Lafferty, William Michael
LOCATION: USA
ASSIGNEE: Diversa Corporation
PATENT: PCT International ; WO 200231203 A2 DATE: 20020418
APPLICATION: WO 2001US31806 (20011010) *US 685432 (20001010) *US 738871 (20001215) *US 790321 (20010221) *US 894956 (20010627) *US PV309101 (20010731)
PAGES: 229 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A
DESIGNATED COUNTRIES: AE; AG; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; BZ; CA; CH; CN; CO; CR; CU; CZ; DE; DK; DM; DZ; EC; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MA; MD; MG; MK; MN; MW; MX; MZ; NO; NZ; PH; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; TZ; UA; UG; US; UZ; VN; YU; ZA; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW; MZ; SD; SL ; SZ; TZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; TR; BF; BJ; CF; CG; CI; CM; GA; GN; GQ; GW; ML; MR; NE; SN; TD; TG

14/3,AB/32 (Item 3 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

136275712 CA: 136(18)275712f PATENT
Methods for synthesizing reporter labeled beads
INVENTOR(AUTHOR): Basiji, David; Ortyn, William
LOCATION: USA
ASSIGNEE: Amnis Corporation
PATENT: PCT International ; WO 200231501 A1 DATE: 20020418
APPLICATION: WO 2001US42639 (20011012) *US PV240125 (20001012) *US PV242734 (20001023)
PAGES: 33 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: G01N-033/53A
DESIGNATED COUNTRIES: AU; CA; JP; US DESIGNATED REGIONAL: AT; BE; CH; CY ; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; TR

14/3,AB/33 (Item 4 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

135300663 CA: 135(21)300663e PATENT
Selection of peptides with antibody-like properties
INVENTOR(AUTHOR): Kodadek, Thomas J.
LOCATION: USA
PATENT: U.S. Pat. Appl. Publ. ; US 20010029024 A1 DATE: 20011011
APPLICATION: US 780575 (20010209) *US PV182060 (20000211)
PAGES: 33 pp. CODEN: USXXCO LANGUAGE: English CLASS: 435007100; G01N-033/53A; C07K-016/18B; C12P-021/08B

14/3,AB/34 (Item 5 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

135195178 CA: 135(14)195178a PATENT
Combinatorial synthesis using mol. wt. differential-based encoding and use in construction of (e.g.) peptide/benzodiazepine libraries

INVENTOR(AUTHOR): Gallop, Mark A.; Dower, William J.; Barrett, Ron W.
LOCATION: USA
ASSIGNEE: Xenoport, Inc.
PATENT: PCT International ; WO 200162772 A2 DATE: 20010830
APPLICATION: WO 2001US5710 (20010222) *US PV184377 (20000223)
PAGES: 79 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C07K-001/00A
DESIGNATED COUNTRIES: AE; AG; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; BZ; CA; CH; CN; CR; CU; CZ; DE; DK; DM; DZ; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MA; MD; MG; MK; MN; MW; MX; MZ; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; TZ; UA; UG; US; UZ; VN; YU; ZA; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW; MZ; SD; SL; SZ; TZ; UG ; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; TR; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

14/3,AB/35 (Item 6 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

134249215 CA: 134(18)249215k PATENT
Substrates and screening methods for transport proteins
INVENTOR(AUTHOR): Dower, William J.; Gallop, Mark; Barrett, Ronald W.; Cundy, Kenneth C.; Chernov-Rogan, Tania
LOCATION: USA
ASSIGNEE: Xenoport, Inc.
PATENT: PCT International ; WO 200120331 A1 DATE: 20010322
APPLICATION: WO 2000US25439 (20000914) *US PV154071 (19990914)
PAGES: 144 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: G01N-033/566A; G01N-033/48B; C12Q-001/68B; C12N-001/68B; C12N-015/63B; C12N-015/85B; C07H-021/04B DESIGNATED COUNTRIES: AE; AG; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; BZ; CA; CH; CN; CR; CU; CZ; DE; DK; DM; DZ; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MA; MD; MG; MK; MN; MW; MX; MZ; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; TZ; UA; UG; US; UZ; VN; YU; ZA; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW; MZ; SD; SL ; SZ; TZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

14/3,AB/36 (Item 7 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

130325397 CA: 130(24)325397f PATENT
Carrier-reporter bead assemblies for solid-phase synthesis of combinatorial libraries
INVENTOR(AUTHOR): Trau, Mathias; Bryant, Darryn Edward
LOCATION: Australia
ASSIGNEE: The University of Queensland
PATENT: PCT International ; WO 9924458 A1 DATE: 19990520
APPLICATION: WO 98AU944 (19981112) *AU 97328 (19971112)
PAGES: 82 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C07K-001/10A; C07K-017/08B; C07K-017/10B; C07K-017/12B; C07K-017/14B; C08J-003/02B
DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN;

YU; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE ; LS; MW; SD; SZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

14/3,AB/37 (Item 1 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

02061678 SUPPLIER NUMBER: 83139515 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Gene therapy of human disease. (Reviews in Molecular Medicine).
Balicki, Danuta; Beutler, Ernest
Medicine, 81, 1, 69(18)
Jan,
2002
PUBLICATION FORMAT: Magazine/Journal; Refereed ISSN: 0025-7974
LANGUAGE: English RECORD TYPE: Fulltext TARGET AUDIENCE: Professional
WORD COUNT: 17268 LINE COUNT: 01480

14/3,AB/38 (Item 2 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01845068 SUPPLIER NUMBER: 55124449 (USE FORMAT 7 OR 9 FOR FULL TEXT)
A Novel N-Aryl Tyrosine Activator of Peroxisome Proliferator-Activated Receptor-(Gamma) Reverses the Diabetic Phenotype of the Zucker Diabetic Fatty Rat.
Brown, Kathleen K.; Henke, Brad R.; Blanchard, Steven G.; Cobb, Jeff E.; Mook, Robert; Kaldor, Istvan; Kliewer, Steven A.; Lehmann, Jurgen M.; Lenhard, James M.; Harrington, Wallace W.; Novak, Paul J.; Faison, Walter; Binz, Jane G.; Hashim, Mir A.; Oliver, William O.; Brown, H. Roger; Parks, Derek J.; Plunket, Kelli D.; Tong, Wei-Qin; Menius, J. Alan; Adkison, Kimberly; Noble, Stewart A.; Willson, Timothy M.
Diabetes, 48, 7, 1415
July,
1999
PUBLICATION FORMAT: Magazine/Journal; Refereed ISSN: 0012-1797
LANGUAGE: English RECORD TYPE: Fulltext TARGET AUDIENCE: Professional
WORD COUNT: 9158 LINE COUNT: 00821

14/3,AB/39 (Item 3 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01195300 SUPPLIER NUMBER: 07385742 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Genetic engineering of filamentous fungi.
Timberlake, William E.; Marshall, Margaret A.
Science, v244, n4910, p1313(5)
June 16,
1989
PUBLICATION FORMAT: Magazine/Journal ISSN: 0036-8075 LANGUAGE: English
RECORD TYPE: Fulltext TARGET AUDIENCE: Academic
WORD COUNT: 4721 LINE COUNT: 00462

14/3,AB/40 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0291649 DBR Accession No.: 2002-13496 PATENT
New SPAS-1 protein or antigen obtained from TRAMP-C2 tumor cells, useful as vaccine for treating or inhibiting cancer in patient, e.g. prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney or germ cell cancer - vector-mediated gene transfer, expression in dendrite cell and macrophage for cancer diagnosis, therapy and recombinant vaccine
AUTHOR: ALLISON J P; FASSO M; SHASTRI N
PATENT ASSIGNEE: UNIV CALIFORNIA 2002
PATENT NUMBER: WO 200224739 PATENT DATE: 20020328 WPI ACCESSION NO.: 2002-362424 (200239)
PRIORITY APPLIC. NO.: US 234472 APPLIC. DATE: 20000921
NATIONAL APPLIC. NO.: WO 2001US28621 APPLIC. DATE: 20010913
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - An isolated polypeptide comprising an immunogenic portion of a SPAS-1 protein, or its variant that differs one or more substitutions, deletions, additions or insertions, where the SPAS-1 protein comprises an amino acid sequence that is encoded by a partial (995 base pairs) or full length (1185 base pairs) SPAS-1 cDNA from TRAMP-C2 tumor cells, or their complements, is new. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an isolated SPAS-1 polynucleotide comprising: (a) the bp sequence cited above; (b) a polynucleotide that: (i) hybridizes under stringent hybridization conditions to (a); (ii) encodes the polypeptide with the sequence having 331 or 395 amino acids fully defined in the specification, or its allelic variant or homologue; or encodes a polypeptide with at least 15 contiguous residues of the amino acid sequence cited above; or (iii) has at least 15 contiguous bases identical to or exactly complementary the bp sequence cited above; (c) a polynucleotide encoding at least 15 amino acid residues of a SPAS-1 protein, or its a variant that differs in one or more substitutions, deletions, additions or insertions, where the tumor protein comprises the amino acid sequence cited above or their complement; or (d) a polynucleotide encoding a SPAS-1 protein or its variant; (2) a vector comprising the polynucleotide or an expression vector comprising the polynucleotide in which the nucleotide sequence is operatively linked with a regulatory sequence that controls expression of the polynucleotide in a host cell; (3) a host cell comprising the polynucleotide, or progeny of the cell; (4) producing the polypeptide; (5) an isolated antibody or its antigen-binding fragment that specifically binds to at least an immunogenic portion of the SPAS-1 human homolog polynucleotides sequence or its complement; (6) a fusion protein comprising at least an immunogenic portion of the SPAS-1 human homolog polypeptide sequence; (7) an isolated polynucleotide encoding the fusion protein; (8) pharmaceutical compositions comprising a pharmaceutical *carrier"** or excipient, and: (a) at least an immunogenic portion of the SPAS-1 human homolog polynucleotides sequence (GenBank Accession Number AF257319); (b) the antibody or its fragment; (c) an antigen-presenting cell that expresses at least an immunogenic portion of the SPAS-1 human homolog polypeptide; (d) the fusion protein; or (e) the polynucleotide encoding the fusion protein; (9) vaccines comprising: (a) at least an immunogenic portion of the SPAS-1 human homolog polynucleotides sequence or its complements, and/or DNA sequences that hybridize to the SPAS-1 human homolog

polynucleotide sequence; and a non-specific immune response enhancer; or (b) an antigen-presenting cell that expresses at least an immunogenic portion of the SPAS-1 human homolog polypeptide sequence, in combination with a non-specific immune response enhancer; (10) removing tumor cells from a biological sample by contacting a biological sample with T cells that specifically react with the SPAS-1 human homolog protein; (11) stimulating T cells specific for the SPAS-1 protein comprising contacting T cells with one or more of the following: (a) at least an immunogenic portion of the SPAS-1 human homolog polypeptide; (b) the polynucleotide encoding the SPAS-1 human homolog polypeptide; or (c) an antigen presenting cell that expresses the SPAS-1 human homolog polypeptide; (12) an isolated T cell population comprising T cells prepared by the method of (11); (13) inhibiting the development of a cancer in a patient; (14) determining the presence or absence of a cancer in a patient; (15) monitoring the progression of a cancer in a patient; and (16) a diagnostic kit, comprising: (a) one or more of the antibodies cited above; and (b) a detection reagent comprising a *reporter"** group. BIOTECHNOLOGY - Preferred Polynucleotide: The polynucleotide may be a DNA molecule comprising a nucleotide sequence encoding the polypeptide above. Specifically, the DNA molecule encodes the SPAS-1 protein. Preferred Method: Producing the polypeptide comprises culturing the host cell so that the polypeptide is expressed and recovering the polypeptide from the cultured host cell or its cultured medium. The host cell is a eukaryote. In method (10), the biological sample is blood or a fraction of it. In method (13), inhibiting the development of a cancer in a patient comprises: (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component consisting of: (i) at least an immunogenic portion of the SPAS-1 human homolog polypeptide; (ii) the polynucleotide encoding the polypeptide; or (iii) an antigen-presenting cell that expresses the polypeptide; such that T cells proliferate; and (b) administering to the patient the proliferated T cells, thus inhibiting the development of a cancer in the patient. The method also involves cloning at least one proliferated cell after performing step (a), and administering to the patient the cloned T cells. In method (14), determining the presence or absence of a cancer in a patient comprises: (a) contacting a biological sample obtained from a patient with a binding agent that binds to the SPAS-1 human homolog protein; (b) detecting in the sample the amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide to a predetermined cut-off value, and from it determining the presence or absence of a cancer in the patient. The binding agent is an antibody, specifically a monoclonal antibody. The method may also comprise: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide encoding the SPAS-1 human homolog protein; (b) detecting in the sample an amount of polynucleotide that hybridizes to the oligonucleotide; and (c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and from it determining the presence or absence of a cancer in the patient. The amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction (PCR) or a hybridization assay. In method (15), monitoring the progression of a cancer in a patient comprises: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to the SPAS-1 human homolog protein; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a

subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b). The method also involves: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide encoding the SPAS-1 human homolog protein; (b) detecting in the sample an amount of polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b). Preferred Compositions: The vaccine comprises a non-specific immune response enhancer, specifically an adjuvant. The non-specific immune response enhancer induces a predominantly Type I response. The antigen-presenting cell is a dendritic cell or a macrophage. The fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with the polynucleotide encoding the fusion protein. Preferred Kit: The detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin. The *reporter"** group comprises radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin or dye *particles"**. ACTIVITY - Cytostatic. No clinical tests described. MECHANISM OF ACTION - Vaccine. USE - The immunogenic portion of the SPAS-1 human homolog polynucleotides sequence, the antibody or its antigen-binding fragment, the antigen-presenting cell, the T cell population and the pharmaceutical compositions are useful for inhibiting the development of a cancer in a patient, specifically prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney, chronic lymphocytic leukemia or germ cell cancer (claimed). In particular, these compounds are useful for as vaccines for inducing protective immunity against cancer. The above mentioned compounds or compositions are also useful for diagnosing cancer and monitoring cancer progression. The patients may include humans, dogs, cats, cattle, horses, pigs, monkeys, rabbits, rats or mice. ADMINISTRATION - Administration may be intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical or oral. Dosage is 1 microgram - 5 mg, preferably 100 microgram - 5 mg per kg of host. EXAMPLE - Normal C57/BL6 male mice were immunized with granulocyte macrophage colony stimulating factor (GMCSF)-producing TRAMP-C2 cells and cytotoxic T lymphocyte antigen (CTLA)-4 using standard protocols. A cDNA *library"** was prepared from TRAMP-C2 cells. The *library"** was screened until final confirmation and isolation of the cDNA. DNA from stimulating pools was recycled through the process until a single clone was obtained. This clone was designated SPAS-1 and comprised the following sequence: partial (995 base pairs) or full length (1185 base pairs). Expression cloning of the SPAS-1 protein was performed. The corresponding protein comprised 331 or 395 amino acids. (107 pages)

14/3,AB/41 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0290687 DBR Accession No.: 2002-12534 PATENT
Identifying polynucleotide in liquid phase comprises contacting polynucleotides derived from organism with nucleic acid probe labelled with detectable molecule and identifying polynucleotide - labeled DNA probe and DNA *library"** for DNA detection and high throughput screening
AUTHOR: SHORT J M; KELLER M; LAFFERTY W M

PATENT ASSIGNEE: DIVERSA CORP 2002
PATENT NUMBER: WO 200231203 PATENT DATE: 20020418 WPI ACCESSION NO.: 2002-340184 (200237)
PRIORITY APPLIC. NO.: US 309101 APPLIC. DATE: 20010731
NATIONAL APPLIC. NO.: WO 2001US31806 APPLIC. DATE: 20011010
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - Identifying a polynucleotide in a liquid phase comprises contacting polynucleotides derived from at least one organism with at least one nucleic acid probe labelled with detectable molecule so that the probe is hybridized to the polynucleotides having complementary sequences and identifying a polynucleotide with an analyzer to detect the detectable molecule. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1) identifying a polynucleotide encoding a polypeptide which comprises coencapsulating in a microenvironment a *library"** of clones containing DNA obtained from a mixed population of organisms with a mixture of oligonucleotide probes comprising a detectable label and at least a part of a polynucleotide sequence encoding a polypeptide having a specified bioactivity under conditions and for a time to allow interaction of complementary sequences and identifying clones containing a complement to the oligonucleotide probe encoding the polypeptide by separating clones with an analyzer to detect the detectable label; (2) high throughput screening of a polynucleotide *library"** for a polynucleotide that encodes a molecule which comprises contacting a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms with oligonucleotides probes labelled with a detectable molecule and separating clones with an analyzer to detect the molecule; (3) screening for a polynucleotide encoding an activity which comprises: (a) normalizing polynucleotides obtained from an environmental sample; (b) generating a *library"** from the polynucleotides; (c) contacting the *library"** with oligonucleotide probes comprising a detectable label and at least a part of a polynucleotide sequence encoding a polypeptide having a specified activity to select *library"** clones positive for a sequence and (d) selecting clones with an analyzer to detect the label; (4) screening polynucleotides which comprises contacting a *library"** of polynucleotides derived from a mixed population of organisms with a probe oligonucleotide labelled with a fluorescence molecule which fluoresces upon binding of the probe to a target polynucleotide of the *library"** to select *library"** polynucleotides positive for a sequence, separating *library"** members that are positive for the sequence with a fluorescent analyzer to detect fluorescence and expressing the selected polynucleotides to obtain polypeptides; (5) obtaining an organism from a mixed population of organisms in a sample which comprises encapsulating at least one organism from the sample in a microenvironment, incubating under conditions and for a time to allow the organism to grow or proliferate and sorting the organism by a flow cytometer; (6) identifying a bioactivity or biomolecule which comprises transferring a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms to a first host cell, contacting the cell with a second host cell containing a detectable *reporter"** molecule in a microenvironment and separating clones with an analyzer to detect the molecule; (7) identifying a bioactivity or biomolecule which comprises transferring a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms to a first host cell, contacting the cell with a second host cell containing a detectable *reporter"** molecule in a microenvironment and optionally separating

clones with an analyzer to detect the molecule; (8) identifying a bioactivity or biomolecule which comprises transferring the extract of a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms to a first host cell and contacting the extract with a second host cell containing a detectable *reporter"** molecule; (9) identifying a bioactivity or biomolecule which comprises transferring the extract of a *library"** containing clones comprising polynucleotides derived from a mixed population of organisms through a column, transferring the extract to a first host cell, contacting the extract with a second host cell containing a detectable *reporter"** molecule and measuring the mass spectra of the host cell with the extract; (10) a sample screening apparatus which comprises an array of capillaries comprising at least one wall defining a lumen for retaining a sample, interstitial material between capillaries and at least one reference indicia formed within the interstitial material; (11) a capillary for screening a sample which comprises a first wall defining a lumen for retaining the sample and forming a waveguide for propagating detectable signals and a second wall formed of a filtering material for filtering excitation energy to the lumen to excite the sample; (12) a capillary array for screening samples which comprises capillaries as above; (13) incubating a bioactivity or biomolecule which comprises introducing a first component into at least a part of a capillary of a capillary array, introducing air into the capillary behind the first component and introducing a second component into the capillary; (14) incubating a sample which comprises introducing a first liquid labelled with a detectable *particle"** into a capillary of a capillary array, optionally with at least one wall coated with a binding material, submersing one end of the capillary into a fluid bath containing a second liquid and evaporating the first liquid; (15) incubating a sample which comprises introducing a liquid labelled with a detectable *particle"** into a capillary of a capillary array, introducing paramagnetic *beads"** to the liquid and exposing the capillary containing the *beads"** to a magnetic field; (16) recovering a sample from one capillary in an array which comprises determining a coordinate position of a recovery tool, detecting a coordinate location of a capillary containing the sample, correlating, via relative movement between the recovery tool and the capillary containing the sample, the coordinate position of the recovery tool with the location of the capillary and contacting the capillary and recovery tool; (17) a recovery apparatus which comprises a recovery tool to contact at least one capillary and recover a sample and an ejector, connected with the recovery tool, for ejecting the sample from the tool; (18) a sample screening apparatus which comprises capillaries in an array, interstitial material and at least one reference indicia formed within the interstitial material, and (19) enriching a polynucleotide encoding an activity which comprises contacting a mixed population of polynucleotides derived from a mixed population of organisms with at least one nucleic acid probe. BIOTECHNOLOGY - Preferred Components: The polynucleotides are from a mixed population of cells. The polynucleotides are in a *library"**, preferably an expression *library"**, especially an environmental expression *library"**. The nucleic acid probe has 15-10000 bases. The detectable molecule is a fluorescent or magnetic molecule. The detectable molecule modulates a magnetic field or the dielectric signature of the clone. The analyzer is a fluorescence activated cell sorting apparatus, a magnetic field sensing device, preferably a Superconducting Quantum Interference Device, a multipole coupling spectroscopy device or flow cytometer. The organism is from an environmental sample, preferably geothermal fields,

hydrothermal fields, acidic soils, sulfotara mud pots, boiling mud pots, pools, hot springs, geysers, marine actinomycetes, metazoan, endosymbionts, ectosymbionts, tropical soil, temperate soil, arid soil, compost piles, manure piles, marine sediments, freshwater sediments, water concentrates, hypersaline sea ice, supercooled sea ice, artic tundras, Sargasso sea, open ocean pelagic, marine snow, microbial mats, whale falls, springs, hydrothermal vents, insect and nematode gut microbial communities, plant endophytes, epiphytic water samples, industrial sites or ex situ enrichments. The environmental sample comprises eukaryotes, prokaryotes, myxobacteria (epothilone), air, water, sediment soil or rock and also contains extremophiles, preferably hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles or acidophiles. The organism comprises a microorganism. The polynucleotide is encapsulated in a microenvironment comprising *beads"** , high temperature agaroses, gel microdroplets, cells, ghost red blood cells, macrophages or liposomes. The detectable molecule is a biotinylated substrate, preferably comprising a spacer connected to a fluorophore structure by a first connector and connected to the bioactivity or biomolecule by a second connector and two groups attached to the fluorophore structure by a connector unit. The fluorophore comprises coumarins, resorufins or xanthenes. The spacer comprises alkanes or oligoethylene glycols. The connector units comprise ether, amine, amide, ester, urea, thiourea or other groups. The polynucleotide encodes an enzyme, preferably lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases, mono- or di-dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, eposize hydrolases, nitrile hydratases, nitrilases, transaminases, amidases or acylases. The polynucleotide encodes a small molecule. The polynucleotide comprises at least one operon, preferably encoding a complete or partial metabolic pathway, especially polyketide syntheses. The *reporter"** system is a bioactive system, preferably C12FDG and also comprising a lipophilic tail, or comprises a detectable label. The *reporter"** system comprises a first test protein linked to a DNA binding group and a second protein linked to a transcriptions activation group. The first and second host cells are prokaryotic or eukaryotic cells. The prokaryotic cell is a bacterial cell and the eukaryotic cell is a mammalian cell. USE - Used for screening for polynucleotides, proteins and small molecules using high throughput of multiple samples. ADVANTAGE - Rapid sorting and screening of *libraries"** from a mixed population of organisms may be effected. EXAMPLE - No relevant example is given.(228 pages)

14/3,AB/42 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0288601 DBR Accession No.: 2002-10448 PATENT
Ovarian tumor polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer - vaccinia virus vector and liposome-mediated recombinant protein gene transfer and expression in host cell for ovary cancer diagnosis and gene therapy
AUTHOR: XU J; STOLK J A; ALGATE P A; FLING S P
PATENT ASSIGNEE: XU J; STOLK J A; ALGATE P A; FLING S P 2002
PATENT NUMBER: US 20020004491 PATENT DATE: 20020110 WPI ACCESSION NO.: 2002-171027 (200222)
PRIORITY APPLIC. NO.: US 825294 APPLIC. DATE: 20010403

NATIONAL APPLIC. NO.: US 825294 APPLIC. DATE: 20010403
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - An isolated ovarian tumor polypeptide (I) comprising a sequence (S1) of 55, 67, 73, 787, 453 or 141 amino acids fully defined in the specification, is new. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an isolated polynucleotide (II) comprises a sequence selected from: (a) a sequence (S2) selected from 84 sequences having 396 base pairs (bp), and a sequence of 924, 3321, 487, 3999, 1069, 1817, 2382, 2377, 1370, 2060, 3000, 1409, 447, 707, 552, 449, 606, 369, 2008, 2364, 1362, 625, 1619, 1010, 480 or 1897 bp fully defined in the specification; (b) complements of (S2); (c) sequences consisting of at least 20 contiguous residues of (S2); (d) sequences that hybridize to (S2) under moderately stringent conditions; (e) sequences having at least 75% preferably 90% identity to (S2); and (f) degenerate variants of (S2); (2) an isolated polypeptide (III) encoded by (II) comprises a sequence from a sequence (S1); sequences encoded by (II); and sequences having 70% preferably 90% identity to sequence encoded by (II); (3) an expression vector (IV) comprising (II) operably linked to a expression control sequence; (4) a host cell transformed or transfected with (IV); (5) an isolated antibody (Ab), or its antigen binding fragment specific to (III); (6) detecting (M1) an ovarian cancer in a patient, comprising contacting a biological sample from the patient with a binding agent that binds to (III), detecting amount of (III) bound to the binding agent, and comparing the amount to a predetermined cut-off value; (7) a fusion protein (V) comprising (III); (8) an oligonucleotide (OLI) that hybridizes to (S2) under moderately stringent conditions; (9) stimulating and/or expanding (M2) T-cells specific for a tumor protein comprising contacting T-cells with (II), (III) or antigen presenting cells (APC) that express (II); (10) an isolated T-cell population (VI) comprising T-cells prepared by M2; (11) a composition (C1) comprising *carriers"** , immunostimulants, and (I), (II), Ab, (IV), (V) or APC; (12) a diagnostic kit comprising OLI, or Ab and detection reagent comprising a *reporter"** group; and (13) inhibiting (M3) the development of a cancer in a patient comprising incubating CD4+ and/or CD8+ T cells isolated from a patient with (III), (II) or APC, such that T cell proliferate, and administering to the patient the proliferated T cells. WIDER DISCLOSURE - Also disclosed are: (1) fragments and/or derivatives of (I); (2) monitoring a progression of a cancer in a patient; (3) polynucleotide compositions comprising antisense oligonucleotides; (4) peptide nucleic acids comprising (II); (5) and (5) binding agents specific to (I). BIOTECHNOLOGY - Preparation: (I) is prepared by standard recombinant techniques. ACTIVITY - Cytostatic. No biodata is given in the source material. MECHANISM OF ACTION - Vaccine; Gene therapy. USE - M1 is useful for detecting a cancer in a patient; M2 is useful for stimulating and/or expanding T-cells specific for a tumor protein; and (M3) is useful for inhibiting the development of a cancer in a patient. C1 is useful for stimulating an immune response in a patient and for treating a cancer in a patient. OLI is useful for determining the presence of a cancer in a patient. The method comprises contacting biological sample from the patient with OLI, detecting amount of (II) that hybridizes to OLI, and comparing the amount to a predetermined cutoff value (claimed). (VI) is further useful for removing tumor cells from a biological sample. (II) is useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumor polypeptides in tumor cells. (I), (II), (III) or (V) is useful in

recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Host cells transformed with (II) is useful for preparation of (I). ADMINISTRATION - C1 comprising (II) is administered by viral based sequence, vaccinia-based infection/transfection system, or is delivered as naked DNA or via *particle"** bombardment. C1 is administered through topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular route, or as lipozomes, nanocapsules, *microparticles"**, lipid *particles"** or vesicles. Further C1 can also be administered through intraperitoneal, subcutaneous, intradermal, anal, vaginal or topical route. Dosage of (III) is 25 microg-5 mg/kg. EXAMPLE - Primary ovarian tumor and metastatic ovarian tumor cDNA *libraries"** were each constructed in kanamycin resistant pZErO-(RTM) 2 vector from pools of three different ovarian tumor RNA samples. For the primary ovarian tumor *library"**, the following RNA samples were used: a moderately differentiated papillary serous carcinoma of a 41 year old, a stage IIC ovarian tumor and a papillary serous adenocarcinoma for a 50 years old Caucasian, and for the metastatic ovarian tumor *library"**, the RNA samples used were omentum tissue from: a metastatic poorly differentiated papillary adenocarcinoma with psammoma bodies in a 73 year old, a metastatic poorly differentiated adenocarcinoma in a 74 years old and a metastatic poorly differentiated papillary adenocarcinoma in a 68 year old, where the number of clones in each *library"** was estimated by plating serial dilutions of unamplified *libraries"** . Insert data were determined from 32 primary ovarian tumor clones and 32 metastatic ovarian tumor clones. Four subtraction *libraries"** were constructed in ampicillin resistant pcDNA31 vector. Two of the *libraries"** were from primary ovarian tumors and two were from metastatic ovarian tumors. In each case, the number of restriction enzyme cut within inserts was minimized to generate full length subtraction *libraries"** . Two hybridizations were performed, and notI-cut pcDNA3.1(+) was the cloning vector for the subtracted *library"**. Still further ovarian carcinoma polynucleotide and/or polypeptide sequences identified. Sequences 0574S, 05845 and 0585S represented novel sequences. The remaining sequences exhibited at least some homology with known genomic and/or expression sequence tag (EST) sequences. (131 pages)

14/3,AB/43 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0286735 DBR Accession No.: 2002-08582 PATENT
Novel isolated polypeptide comprising at least an immunogenic portion of herpes simplex virus antigen, useful as component of vaccines used for treating herpes simplex virus infection in a patient - vector-mediated gene transfer, expression in host cell and antisense oligonucleotide for gene therapy
AUTHOR: HOSKEN N A; DAY C H; DILLON D C; MCGOWAN P; SLEATH P R
PATENT ASSIGNEE: CORIXA CORP 2002
PATENT NUMBER: WO 200202131 PATENT DATE: 20020110 WPI ACCESSION NO.: 2002-154689 (200220)
PRIORITY APPLIC. NO.: US 277438 APPLIC. DATE: 20010320
NATIONAL APPLIC. NO.: WO 2001US20981 APPLIC. DATE: 20010628
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - An isolated polypeptide (I) comprising at least an immunogenic portion of an herpes simplex virus (HSV) antigen which comprises one of 28 22-1142 residue amino acid

sequences, fully defined in the specification, is new. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an isolated polynucleotide (II) encoding (I); (2) a fusion protein (III) comprising (I) and a fusion partner; (3) an isolated polynucleotide (IV) encoding (III); (4) an isolated monoclonal or polyclonal antibody or its antigen-binding fragment (V), that specifically binds to (I); (5) a composition (VII) comprising (I), (II) and a *carrier"**; (6) a pharmaceutical composition (a vaccine) (VIII) comprising (I), (II) and an immunostimulant; (7) a diagnostic kit (IX) comprising (I), (III), (V) and a detection reagent; (8) a pharmaceutical composition (X) for the treating of HSV infection in a patient, comprising T cells proliferated in the presence of (I), in combination with a *carrier"**; (9) treating (M1) HSV infection in a patient by incubating antigen presenting cells (APC) in the presence of (I), which are then administered to the patient; and (10) a pharmaceutical composition (XI) for treating HSV infection in a patient comprising APC incubated in the presence of (I), in combination with a *carrier"**. WIDER DISCLOSURE - Disclosed as new are the following: (1) an isolated polypeptide comprising a variant or biologically functional equivalent of the immunogenic portion of a HSV antigen; (2) polypeptides encoded by sequences that hybridize to (II) or its complement; (3) expression vectors comprising (II); (4) host cells transformed or transfected with the expression vectors comprising (II); (5) polynucleotide and polypeptide sequences having substantial identity to the above mentioned sequences; (6) polynucleotides complementary to (II); and (7) antisense oligonucleotide sequences that specifically bind to (II) or its complement. BIOTECHNOLOGY - Preferred Polypeptide: (I) preferably comprises an immunogenic portion of HSV UL46 (e.g. GlyArgValTyrGluGluIleProTrpValArgValTyrGluAsn, TyrGluAsnIleCysLeuArgArgGlnThrAlaGlyGlyAlaAla, ProAspSerProTyrIleGluAlaGluAsnProLeuTyrAspTrp, TyrIleGluAlaGluAsnProLeuTyrThrTrpGlyGlySerAla, ThrAsnAlaLeuAlaAsnAspGlyProThrAsnValAlaAlaLeu, ArgValLeuProThrArgIleValAlaCysProValAspLeuGly, ThrArgIleValAlaCysProValAspLeuGlyLeuThrHisAla, GluGluIleProTrpValArgValTyrGlyAsnIleCysProArg, ProGlyThrAlaProAspSerProTyrIleGluAlaGluAsnPro, ProAspSerProTyrIleGluAlaGluAsnProLeuTyrAspTrp, or GluAsnProLeuTyrAspTrpGlyGlySerAlaLeuPheSerPro), HSV UL15 (e.g. SerProAsnThrAspValArgMetTyrSerGlyLysArgAsnGly, or TyrLeuAlaAlaProThrGlyIleProProAlaPhePheProIle), HSV US3 (e.g. AlaIleAspTyrValHisCysGluGlyIleIleHisArgAspIle), HSV US8A (e.g. AlaPheProValAlaLeuHisAlaValAspAlaProSerGlnPhe) antigen, where the HSV UL46, HSV UL15, HSV US3 or HSV US8A antigens have a 722, 734, 481, or 146 residue amino acid sequence, respectively, all fully defined in the specification. Preferred Fusion Protein: (III) comprises (I) and a fusion partner which: (a) is expression enhancer that increases expression of (III) in a host cell transfected with polypeptide encoding (III); (b) comprises a T helper epitope that is not present within (I); or (c) comprises an affinity tag. Preferred Composition: (VIII) comprises an immunostimulant such as monophosphoryl lipid A, aminoalkyl glucosaminide phosphate saponin, or its combination. Preferred Kit: (IX) comprises (I) immobilized on a solid support, a detection reagent which comprises a *reporter"** group (e.g., radioisotope, fluorescent group, luminescent group, enzyme, biotin or dye *particle"**) conjugated to a binding agent such as an anti-immunoglobulin, protein G, protein A or lectin. Preferred Method: In M1, APC such as dendritic cells, macrophage cells, B cells, fibroblast cells, monocyte cells, and stem cells are incubated with (I). ACTIVITY - Virucide. MECHANISM OF ACTION - Vaccine. No biological data is given. USE - (I) is useful for detecting human immunodeficiency virus (HIV) infection in a patient which involves detecting the

presence of antibodies that bind to (I) which is contacted with a biological sample (e.g. whole blood, serum, plasma, saliva, cerebrospinal fluid or urine) obtained from a patient. (I) is also useful for treating HSV infection in a patient which involves incubating peripheral blood cells obtained from the patient in the presence of (I) such that T cells proliferate, and then administering the proliferated T cells to the patient. The T cells are incubated one or more times. Preferably, T cells are separated from the peripheral blood cells obtained from the patient, and incubated in the presence of (I). The obtained T cells are further separated into CD4+ cells or CD8+ T cells from the peripheral blood cells, and are incubated in presence of (I) such that they proliferate. The method further involves separating gamma/delta T lymphocytes from the peripheral blood cells, and proliferating them in the presence of (I). Incubation of the obtained peripheral blood cells further involves cloning one or more T cells that proliferated in the presence of (I). (V) which is capable of binding (I), is useful for detecting HSV infection in a biological sample which involves detecting in the sample, a polypeptide that binds to (V). (VII) and (VIII) are useful for stimulating immune response in a patient. (All claimed). (II) is useful as probes and primers for nucleic acid hybridization. The probes and primers are useful for detecting HSV infection in a patient. (X) is useful for removing HSV infected cells from a biological sample. The treated biological sample is then used for inhibiting the development of HSV infection in a patient. ADMINISTRATION - Pharmaceutical compositions comprising (I), (II), T cells or (V) are administered by oral, parenteral, intravenous, intranasal or intramuscular route. Dosage of (I) ranges from 25 micro-g-5 mg/kg of host. EXAMPLE - Identification of herpes simplex virus (HSV)-2 antigens was carried out as follows: Lymphocytes were obtained from two types of donors with unknown clinical status, and group B) seropositive donors with well characterized clinical status (viral shedding and anogenital lesion recurrences). Cryopreserved peripheral blood mononuclear cells (PBMCs) or lesion-biopsy lymphocytes were thawed and stimulated in vitro with 1 micro-g/ml HSV-2 antigen. Irradiated autologous PBMC were added as antigen presenting cells for the lesion biopsy lymphocytes only. Recombinant interleukin (IL)-2 was added on days 1 and 4. The cells were harvested, washed and replated in fresh medium containing IL-2 and IL-7 on day 7. Recombinant IL-2 was again added on day 10. The T cells were harvested, washed and restimulated in vitro with HSV-2 antigen plus irradiated autologous PBMC in the same manner on day 14 of culture. The T cell lines were cryopreserved at 1x10 to the power 7 cells/vial in liquid nitrogen on day 11-12 of the secondary stimulation. After thawing, the cryopreserved T cells retained the ability to specifically proliferate to HSV-2 gene fragment expression cloning *libraries"** prepared in Escherichia coli. HSV-2 (333) DNA was prepared. The HSV2-1 *library"** was constructed as follows: DNA fragments were generated by sonicating genomic HSV-2 DNA for 4 seconds. The sonicated DNA was then precipitated, pelleted, and resuspended in 11 micro-l TE buffer. The average size of the DNA fragments was determined to be approximate. 500 base pair when visualized after ethidium bromide staining of the gel. Incomplete DNA fragment ends were filled in using T4 DNA polymerase. EcoRI adapters were then ligated to the blunt ends of the DNA fragments using T4 DNA ligase. The DNA was phosphorylated using T4 polynucleotide kinase, purified and ligated into the pET17b expression vector. The HSV2-II *library"** was constructed in similar fashion. The HSV2-1 *library"** was transformed into E. coli for preparation of glycerol stocks and testing of HSV-2 DNA insert representation. The DNA was

transformed into ElectroMAX DH10B E. coli. Transformed bacteria were grown. A small subset of colonies were picked for sequencing of DNA inserts, and the remaining bacteria from each plate collected as a pool for preparation of plasmid DNA. These pools were named HSV-2 pools 9, 10 and 11. Glycerol stocks of a portion of the pools. Equal quantities of plasmid DNA from each of the 3 pools was combined to make a single pool of plasmid DNA. JM109(DE3) bacterial were then transformed with an amount of the final pool of *library"** DNA. The transformed bacteria then plated on 100 LB/amp plates. Twenty colony forming units (CFU) were actually observed on each of the 100 plates. The bacterial colonies were collected as a pool from each plate in 800 micro-l/plate of Luria broth (LB) + 20 % glycerol. Each pool was distributed equally among four 96-well U-button plates and the master stock plate were stored. The size of the HSV-2 gene-fragment *library"** referred to a HSV21 was 96 pools of 20 clones/pools. Plasmid DNA was prepared from 20 randomly picked colonies and the inserts sequenced. Approximately 15% contained HSV-2 DNA as insert, 80 % contained non-HSV-2 DNA, and %% contained no insert DNA. The HSV-2 fragment expression *library"** was induced for screening with human CD4+ T cells. Autologous dendritic antigen presenting cells (APCs) and responder T cells were prepared. The T cells were resuspended in fresh RPMI 1640 + 10 % HS and added at 2x10 to the power 4/well to the plates containing the E. coli-pulsed autologous DC's. After 3 days, 100 micro-l/well of supernatant was removed and transferred to new 96 well plates. The supernatant was subsequently tested for interferon (IFN-gamma) content by enzyme linked immunosorbent assay (ELISA). The T cells were then pulsed with 1 micro-Ci/well of (3H)-thymidine. The 3H-pulsed cells were then harvested onto Unifilter GF/C and the CPM of (3H)-incorporated subsequently measured using a scintillation counter. ELISA assays were performed on cell supernatants following a standard cytokine-capture ELISA protocol for human IFN-g. From the HSV2-I *library"** screening with T cells from D104, wells HSV2I-H10 and HSV2I-H12, for which both CPM and IFN-g levels were significantly above background, were scored as positive. The positive wells (HSV2I-H10 and HSV2I-H12) from the initial CD4+T cell screening experiment were grown up again from the master glycerol stock plate. Forty-eight sub-clones from each pool were randomly picked, grown up. The subclones were screened against the AD104 CD4+T cell line. A clone (HSV2I-H10 and HSV2I-H12) from the HSV21-H12 pool breakdown scored positive. This positive result was verified in second AD104 CD4+T cell assay. An HSV antigen which comprises a 271, 1142, 64, 70, 146, 22, 143, 481, 106, 722, 66, 904, 37, 147, 110, 318, 135, 734, 376, 136, 284, 838, 215, 826, 993, 1113, 1037 or 193 residue amino acid sequence, fully defined in the specification was identified from the positive clones. (157 pages)

14/3,AB/44 (Item 5 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0284747 DBR Accession No.: 2002-06594 PATENT
Generating antibody with selected biological activity involves combining variegated antibody display *library"** in display mode with soluble secreted antibody *libraries"** in secretion mode - antimicobial activity for use in bacterium and fungus infection prevention and therapy
AUTHOR: GYURIS J; MORRIS A; MEIER-EWERT S; NAGY Z
PATENT ASSIGNEE: GPC BIOTECH INC; GPC BIOTECH AG 2002

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PRIORITY APPLIC. NO.: US 214200 APPLIC. DATE: 20000626
NATIONAL APPLIC. NO.: WO 2001US20380 APPLIC. DATE: 20010626
LANGUAGE: English

ABSTRACT: DERWENT ABSTRACT: NOVELTY - Generating antibody (Ab) with selected activity, comprising isolating subpopulation (I) of display packages (DP) enriched for test Abs (T) having binding specificity for cell, from Ab display *library"** having population of (T) expressed on surface of DP population, simultaneously expressing (I) so that (T) is secreted, and assessing ability of secreted (T) to regulate a process in target cell, is new. DETAILED DESCRIPTION - Generating (M1) an Ab with a selected biological activity, comprising: (a) providing an Ab display *library"** comprising a variegated population of (T) expressed on the surface of a population of DP; (b) in a display mode, isolating, from the Ab display *library"**, a subpopulation (I) of DP enriched for (T) which have a desired binding specificity and/or affinity for a cell or its component; (c) in a secretion mode, simultaneously expressing (I) under conditions, where the (T) are secreted and are free of the DP; and (d) assessing the ability of the secreted (T) to regulate a biological process in a target cell. INDEPENDENT CLAIMS are also included for the following: (1) an Ab display *library"** (II) enriched for (T) having a desired binding specificity and/or affinity for a cell or its component and which regulate a biological process in a target cell; (2) a vector (III) comprising a chimeric gene (CG) for a chimeric protein, where the chimeric gene comprises: (a) a coding sequence for a (T); (b) a coding sequence for a surface protein of a DP; and (c) RNA splice sites flanking the coding sequence for the surface protein, where in a display mode, the chimeric gene is expressed as a fusion protein including (T) and the surface protein, so that the (T) can be displayed on the surface of a population of DP, whereas in the secretion mode, the (T) is expressed without surface protein as a result of the coding sequence for the surface protein being removed by RNA splicing; (3) a vector *library"** (IV), where each vector is (III), and the vector *library"** collectively encodes the variegated population of (T); (4) a cell composition (V) comprising a population of cells containing (IV); (5) preventing or treating infection of an animal by a microorganism involves administering to the animal a pharmaceutical preparation which comprises one or more (T) or peptidomimetic of (T) that inhibits growth of the target microorganism e.g. bacteria or fungi, where the (T) is generated by using (M1); (6) modulating an angiogenic process in a mammal involves administering to the animal a pharmaceutical preparation comprising peptidomimetics of one or more (T) that inhibit proliferation of endothelial cells in the presence of an angiogenic amount of an endogenous growth factor; and (7) a construct pAM6 M13/COS peptide expression plasmid, pAM7 and pAM9 M13/COS peptide expression plasmid, or pAM8 M13/COS peptide expression plasmid, pAM7. BIOTECHNOLOGY - Preferred Method: The Ab display *library"** is a phage display *library"**. Preferably, the population of (T) is expressed on surface of population of phage *particles"** such as M13, f1, fd, If1, Ike, Xf, Pf1, Pf3, lambda, T4, T7, P2, P4, phiX-174, MS2 or f2. Optionally, the phage display *library"** is generated with a filamentous bacteriophage (M13, fd or f1) specific for Escherichia coli and the phage coat protein is coat protein III or coat protein VIII. Optionally, the Ab display *library"** is a bacterial cell-surface display *library"** or a spore display *library"**. (T) are enriched from the Ab display *library"** in the display mode by a differential binding means which involves affinity separation of (T)

which specifically bind the cell or its component from (T) which do not. Preferably, the (T) are enriched from Ab display *library"** by: (a) panning the Ab display *libraries"** on whole cells; (b) by affinity chromatography in which a component of a cell is provided as part of an insoluble matrix which comprises a cell surface protein attached to a polymeric support; or (c) immunoprecipitating DP. In (M1), the display mode enriches for (T) that bind to cell-type specific marker or for (T) that bind to a cell surface receptor protein e.g. G-protein coupled receptor (chemoattractant Ab receptor, a neuroantibody receptor, a light receptor, a neurotransmitter receptor, a cyclic AMP receptor, or a polypeptide hormone receptor), such as alpha1A-adrenergic receptor, alpha1B-adrenergic receptor, alpha2-adrenergic receptor, alpha2B-adrenergic receptor, beta1-adrenergic receptor, beta2-adrenergic receptor, beta3-adrenergic receptor, m1 acetylcholine receptor (AChR), m2 AChR, m3 AChR, m4 AChR, m5 AChR, D1 dopamine receptor, D2 dopamine receptor, D3 dopamine receptor, D4 dopamine receptor, D5 dopamine receptor, A1 adenosine receptor, A2b adenosine receptor, 5-HT1a, 5-HT1b, 5HT1-like, 5-HT1d, 5HT1d-like, 5HT1d beta, substance K (neurokinin A), fMLP receptor, fMLP-like receptor, angiotensin II type 1 receptor, endothelin ETA receptor, endothelin ETB receptor, thrombin receptor, growth hormone-releasing hormone (GHRH) receptor, vasoactive intestinal Ab receptor, oxytocin receptor, somatostatin SSTR1 and SSTR2 receptor, SSTR3 receptor, cannabinoid receptor, follicle stimulating hormone (FSH) receptor, leutropin (leutinizing hormone (LH)/human chorionic gonadotrophin (HCG)) receptor, thyroid stimulating hormone (TSH) receptor, thromboxane A2 receptor, platelet-activating factor (PAF) receptor, C5a anaphylatoxin receptor, interleukin 8 (IL-8) IL-8RA receptor, IL-8RB receptor, Delta Opioid receptor, Kappa Opioid receptor, mip-1/RANTES receptor, Rhodopsin receptor, Red opsin receptor, Green opsin receptor, Blue opsin receptor, metabotropic glutamate mGluR1-6 receptor, histamine H2 receptor, ATP receptor, neuroantibody Y receptor, amyloid protein precursor receptor, insulin-like growth factor II receptor, bradykinin receptor, gonadotropin-releasing hormone receptor, cholecystokinin receptor, melanocyte stimulating hormone receptor, antidiuretic hormone receptor, glucagon receptor, or adrenocorticotropic hormone II receptor. Optionally, the display mode enriches for test antibodies that bind to: (a) receptor tyrosine kinase, preferably an EPH receptor such as eph, elk, eck, sek, mek4, hek, hek2, eek, erk, tyro1, tyro4, tyro5, tyro6, tyro11, cek4, cek5, cek6, cek7, cek8, cek9, cek10, bsk, rtk1, rtk2, rtk3, myk1, myk2, ehk1, ehk2, pagliaccio, htk, erk or nuk receptor; (b) a cytokine receptor; or (c) multisubunit immune recognition receptor (MIRR) receptor. The Ab display *library"** provided in (M1) comprises at least 103 different (T) that are single chain antibodies. Each (T) is encoded by a CG as described above. The CG further comprises a coding sequence for Ab dimerization sequence, where the (T) dimerize upon secretion. (T) are expressed by a eukaryotic cell e.g. mammalian cell in a secretion mode. The secreted (T) are assessed for their ability to regulate a biological process such as a change in cell differentiation, cell proliferation or cell death, in a target mammalian cell, preferably human cell. The biological process is detected by changes in intracellular calcium mobilization, intracellular protein phosphorylation, changes in phospholipid metabolism or by changes in expression of cell-specific marker genes. The display mode enriches for test antibodies that bind to a target cell surface protein, where the target cell further comprises a *reporter"** gene construct containing a *reporter"** gene in operative linkage with one or more

transcriptional regulatory elements responsive to the signal transduction activity of the cell surface receptor protein, expression of the *reporter"** gene providing the detectable signal. The *reporter"** gene encodes a product that gives rise to a detectable signal such as color, fluorescence, luminescence, cell viability, relief of a cell nutritional requirement, cell growth or drug resistance. Preferably, the *reporter"** gene encodes a gene product such as chloramphenicol acetyl transferase, beta-galactosidase or secreted alkaline phosphatase, or a *reporter"** gene that encodes a gene product conferring a growth signal. In (M1), the secretion mode involves assessing the ability of the secreted (T) to inhibit the biological activity of an exogenously added compound on target cells, e.g. the DP which bind to endothelial cells are isolated, and the ability of the secreted (T) to inhibit proliferation of endothelial cells is assessed in the presence of an angiogenic amount of an endogenous growth factor. (M1) further involves formulating, with a *carrier"** , one or more (T) that regulate the biological process in the target cell. (M1) further involves converting one or more (T) that regulate the biological process in a target cell, into peptidomimetics and formulating the peptidomimetics with a *carrier"**. Preferably, the secreted antibodies are dimerized. Preferred Vector: (III) comprises CG which further comprises secretion signal sequences for secretion of (T) in secretion mode, from eukaryotic cells such as mammalian cells. Preferred Vector *Library"**: (IV) collectively encodes at least 103 different single chain (T). ACTIVITY - Antibacterial; Fungicide. No biological data is given. MECHANISM OF ACTION - Target microorganism growth inhibitor. USE - Generating antibody (Ab) with selected biological activity. (M1) is useful for generating Ab with selected antimicrobial activity which involves providing a recombinant host cell population which expresses a soluble Ab *library"** comprising a variegated population of (T). The host cells are cultured with a target microorganism under conditions where the Ab *library"** is secreted and diffuses to the target microorganism. The host cells expressing (T) that inhibit growth of the target microorganism such as a bacteria or fungi, are selected. The host cells employed in the method are bacteria cultured on agar embedded with target microorganisms. The antimicrobial activity of (T) is determined by zone clearing in the agar. The host cell population expresses soluble Ab *library"** comprising 103 different (T) of 4-20 amino acid residues in length. The method further involves converting one or more (T) into peptidomimetics which are formulated with a *carrier"** to inhibit growth of a target microorganism. (All claimed). (M1) is useful for identifying antibodies with antiangiogenic activity, antiproliferative activity, anti-infective antibodies, e.g. which are antifungal or antibacterial agents, for detecting agonists or antagonists of a receptor function and to test functional ligand-receptor or ligand-ion channel interactions for cell surface-localized receptors and channels. The method can also be used to identify effectors of G-protein coupled receptors, receptor tyrosine kinases, cytokine receptors, and ion channels. ADMINISTRATION - The antibody is administered by topical or systemic route. No dosage is suggested. ADVANTAGE - The display mode and the secretion mode can be carried out without the need to subclone the test antibody coding sequence into another vector, and thus reduces loss of antibody sequences from the sub-*library"**. EXAMPLE - None given. (88 pages)

14/3,AB/45 (Item 6 from file: 357)

0283761 DBR Accession No.: 2002-05608 PATENT
New regulatable, catalytically active nucleic acids (RCANA), useful in gene therapy (particularly for regulating gene expression), or in assays for detecting the presence of ligands or activation of an effector of RCANA - DNA biocatalyst, aptazyme and aptamer for use in gene therapy
AUTHOR: ELLINGTON A D; HESSELBERTH J; MARSHALL K; ROBERTSON M; SOOTER L ; DAVIDSON E; COX J C; REIDEL T
PATENT ASSIGNEE: UNIV TEXAS SYSTEM 2001
PATENT NUMBER: WO 200196559 PATENT DATE: 20011220 WPI ACCESSION NO.: 2002-122216 (200216)
PRIORITY APPLIC. NO.: US 212097 APPLIC. DATE: 20000615
NATIONAL APPLIC. NO.: WO 2001US19302 APPLIC. DATE: 20010614
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - A polynucleotide (I), which is regulated by a peptide, is new, where (I) comprises a regulatable, catalytically active nucleic acid (RCANA) or polynucleotide, where the peptide interacts with (I) to affect its catalytic activity. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) a nucleic acid segment comprising a RCANA, selected from a pool of nucleic acids in which at least one of the catalytic residues has been randomized; (2) a RCANA segment comprising: (a) an effector domain; and (b) a nucleic acid catalyst domain in which one or more critical catalytic residues of the nucleic acid catalyst have been randomized; where the kinetic parameters of the catalytic domain are regulated by an effector that interacts with the effector domain; (3) isolating, making or selecting a RCANA; (4) detecting a target using a RCANA comprising: (a) contacting the RCANA with the target; an (b) measuring the effect of the interaction between the RCANA and the target; (5) modifying a target using a RCANA comprising: (a) providing a RCANA capable of target specific modification; and (b) modifying the target under conditions that cause RCANA-specific activity; (6) biosensors comprising a solid support and at least one RCANA, where the kinetic parameters of the nucleic acids on a target vary in response to the interaction of an effector molecule with the nucleic acid; where: (i) the nucleic acid construct is immobilized on the support; (ii) catalytic targets of the catalytic domain is immobilized on the support; or (iii) the effector is immobilized on the support; (7) detecting an effector comprising: (a) mixing a RCANA, where the kinetic parameters of the nucleic acids on a target vary in response to the interaction of an effector molecule with the nucleic acid with the catalytic target of the nucleic acid and effectors; (b) isolating the RCANA that have reacted with their catalytic targets; and (c) detecting the RCANA that have reacted with their catalytic targets; (8) detecting a RCANA comprising: (a) isolating a RCANA; (b) creating a construct in which the nucleic acid is in a position to regulate the expression of a *reporter"** gene; (c) introducing the construct into a host cell; and (d) measuring the catalytic activity of the nucleic acid upon exposure of the host cell to an effector; (9) vectors comprising: (a) a RCANA, where the peptide molecule interacts with the polynucleotide to affect its catalytic activity; or (b) a RCANA generated by the modification of a catalytic residue; (10) a device for automatically selecting an aptazyme; (11) an automated method for selecting aptamer oligonucleotides; (12) a substrate that produces a signal when an aptazyme reaction occurs comprising a solid support, and at least one aptazyme construct having a regulatable aptamer oligonucleotide

sequence with a regulatory domain, where the kinetic parameters of the aptazyme on a target gene vary in response to the interaction of an allosteric effector molecule with the regulatory domain, and where the aptazyme construct is covalently immobilized on the support; (13) detecting an aptazyme reaction comprising: (a) providing a substrate comprising a solid support and an aptazyme construct or a heterogenous mixture of aptazyme constructs covalently immobilized on the support; (b) providing an analyte; (c) providing a substrate tagged to be detectable; (d) exposing the substrate and an analyte to the immobilized aptazyme, where the substrate is bound to the immobilized aptazyme upon activation of the aptazyme reaction by the analyte to produce a signal; (e) washing unbound substrate off of the substrate; and (f) detecting the signal from the bound substrate; and (14) modulating the expression of a nucleic acid comprising: (a) providing a RCANA; and (b) contacting the polynucleotide with the peptide, thereby modulating expression of a nucleic acid. BIOTECHNOLOGY - Preferred Polynucleotide: The peptide is further defined as being a portion of a protein. The peptide comprises about 7 - 20 amino acids, preferably, about 7 - 12 amino acids. The catalytic activity of the nucleic acid is specific for a nucleic acid target sequence. The catalytic activity of the nucleic acid is regulated by the interaction of the nucleic acid with an effector. The polynucleotide comprises RNA or DNA. The polynucleotide is partially single stranded or partially double stranded. The polynucleotide comprises at least one modified base. The peptide or effector is endogenous or exogenous. In particular, it comprises a phosphorylated peptide. Specifically, the nucleic acid that is regulated by an effector comprising RCANA, is generated by the modification of a catalytic residue. The effector comprises a protein, a pharmaceutical agent, a protein complex, a peptide, a phosphorylated peptide or a dephosphorylated peptide. The nucleic acid catalyzes a reaction that causes the expression of a target gene to be up regulated or down regulated. The nucleic acid is used to detect an exogenous effector from a *library"** of candidate exogenous effector molecules. The nucleic and the effector form a nucleic acid-effector complex. The nucleic acid and the effector is a molecule that forms an nucleic acid-effector complex and the nucleic acid-effector complex acts synergistically to effect the catalytic activity of the nucleic acid-effector complex. The nucleic acid catalyses: (a) a ligation reaction with an oligonucleotide substrate; (b) a reaction that adds a non-oligonucleotide substrate; (c) a reaction that adds biotin to the nucleic acid; or (d) a cleavage reaction with an oligonucleotide substrate. The kinetic parameters of nucleic acid catalysis are altered in the presence of one or more effector-effectors that acts on the effector molecule that interacts with the nucleic acid. The kinetic parameters of nucleic acid catalysis are altered in the presence of theophylline. The kinetic parameters of nucleic acid catalysis are also altered in the presence of a supermolecular structure. In particular, the kinetic parameters of nucleic acid catalysis are altered in the presence of a supermolecular structure that comprises a virus *particle"** or a cell wall. The nucleic acid comprises a gene and a RCANA inserted within the gene, where the presence of an effector causes the nucleic acid to catalyze a reaction. In particular, the catalytic reaction is a self-splicing reaction, a ligation reaction or a trans-cleavage reaction. The catalytic activation of the nucleic acid leads to changes in expression of the gene, in the expression of one or more genes, in expression of the mRNA of the gene or in expression of the protein encoded by the gene. Preferred Biosensor: The reaction is machine readable. The solid support comprises a multiwell plate or a

surface plasmon resonance sensor. The RCANA is covalently immobilized on the solid support. The catalytic reaction produces a detectable signal. In particular, the catalytic reaction is the attachment of a tag to the immobilized nucleic acids to produce the signal. The substrate is further defined as containing known nucleic acid sequence tags and the nucleic acids are sorted on the surface of the substrate based on non-covalent hybridization to sequence tags. Preparation: Isolating RCANA comprises: (a) randomizing a nucleotide in the catalytic domain of a catalytically active nucleic acid to create a nucleic acid pool; and (b) removing from the nucleic acid pool those nucleic acids that interact with the catalytic target of the catalytic domain. The method further comprises adding an effector to the remaining (pool of) nucleic acids, where the effector acts on the nucleic acids to alter the catalytic activities of the nucleic acids. The method further comprises purifying the isolated nucleic acid and sequencing the isolated nucleic acid. The step of removing the nucleic acids is under high stringency conditions, moderate stringency conditions or low stringency conditions. The target is an mRNA molecule. The effector is a protein, a peptide, a phosphoprotein, a glycoprotein, light, visible light or a magnet. The target may also be a metabolic reaction. The nucleic acids with altered catalytic specificity are selected in the presence and/or absence of an effector. The effector domain comprises a completely random sequence pool or a partially randomized sequence pool. Isolating a RCANA also comprises: (a) randomizing a nucleotide in the catalytic domain of a catalytically active nucleic acid to create a nucleic acid pool; (b) removing from the nucleic acid pool those nucleic acids that interact with the catalytic target of the catalytic domain; (c) adding an effector molecule to the nucleic acids; and (d) isolating those nucleic acids that interact with the catalytic target of the catalytic domain. Making a RCANA comprises: (a) contacting a pool of nucleic acids, the nucleic acids having a catalytic and an effector domain, where a nucleotide in the catalytic domain of the nucleic acids has been randomized; (b) removing from the nucleic acid pool those nucleic acids that interact with the catalytic target of the catalytic domain; (c) adding an effector protein to the remaining nucleic acids; and (d) isolating those nucleic acids that interact with the catalytic target of the catalytic domain. Preferred Method: Selecting a RCANA comprises: (a) contacting a pool of nucleic acids, the nucleic acids having a catalytic and an effector domain, where a nucleotide in the catalytic domain of the nucleic acids has been randomized; (b) removing from the nucleic acid pool those nucleic acids that interact with the catalytic target of the catalytic domain; (c) adding an effector to the remaining nucleic acids; and (d) isolating those nucleic acids that interact with the catalytic target of the catalytic domain; (e) introducing the nucleic acids into a host cell; and (f) measuring the catalytic activity of the nucleic acid upon exposure of the host cell to the effector. In method (7), the reacted RCANA are isolated by immobilization on a solid support. The reacted RCANA contain a tag sequence or produce a detectable signal. The automated method for selecting aptamer oligonucleotides comprises: (1) providing a programmable robot having a programmable robotic arm adapted for pipetting with disposable pipette tips; (2) providing a work surface accessible to the robot, the work surface having modules including reservoirs for reagents and pipette tips, a magnetic *bead"** separator, an enzyme cooler and a thermal cycler; (3) preparing reagents including random pool RNA, buffers, enzymes, streptavidin magnetic *beads"** and biotinylated targets; (4) providing disposable

pipette tips; (5) preloading each reagent into a designated reservoir for each reagent; (6) preloading pipette tips into a designated reservoir of the work surface; (7) programming the robot to perform a desired selection involving: (a) incubating an RNA pool in the presence of a biotinylated target conjugated to streptavidin magnetic *beads"** and an allosteric effector molecule using a pipette tip equipped robotic arm to combine the components of the incubation mixture; (b) exposing the magnetic *beads"** to the magnetic *bead"** separator upon completion of incubation; (c) separating the *beads"** from the incubation mixture; (d) washing the *beads"** to leave RNA bound to a target attached to the *beads"**; (e) reverse transcribing the bound RNA to produce DNA oligonucleotides; (f) amplifying the DNA oligonucleotides with the enzyme cooler and the thermal cycler; (g) transcribing the DNA oligonucleotides in vitro to produce RNA oligonucleotides; (h) executing the program; and (i) using the RNA oligonucleotide in iterative rounds of selection. The method of (13) is automated and the signal is amplified for detection. Preferably, the aptazyme construct comprises modified nucleotides to inhibit degradation of the aptazyme. In method (14), the polynucleotide is provided in a cell. Preferably, the cell is provided in vitro or in vivo. The cell may be a prokaryotic cell or a eukaryotic cell. Modulating expression of a nucleic acid specifically comprises: (a) providing a RCANA, where the RCANA molecule includes a modified catalytic residue; and (b) contacting the nucleic acid with the effector, thereby modulating expression of a nucleic acid. The device of (10) or the method of (11) is adapted for selection of DNA oligonucleotides, modified RNA oligonucleotides, ribozymes, phage displayed proteins, or cell-surface displayed proteins. The device is used to detect biological warfare agents. Preferably, the aptazyme comprises RNA or DNA. The aptazyme is partially single stranded or partially double stranded. The aptazyme is used to detect an exogenous effector molecule from a *library"** of candidate exogenous effector molecules. The aptazyme and the effector molecule form an aptazyme-effector complex, where the aptazyme-effector complex acts synergistically to effect the catalytic activity of the aptazyme-effector complex. The aptazyme and the effector molecule form a chimeric active site, and where the chimeric active site acts synergistically to effect the activity of the aptazyme. The aptazyme is used to determine the metabolic state of a cell, at least one substance that perturbs cellular metabolism. Preferred Substrate: The substrate is machine readable and comprises a multiwell plate. The substrate further comprises *beads"** in the wells, where the aptazyme is covalently immobilized on the *beads"** . The aptazymes are filter washed. Upon occurrence of an aptazyme reaction in the presence of a detectable tag to be detected, the detectable tag is attached to the immobilized aptazyme to produce the signal. The detectable tag comprises a fluorescent tag. The substrate also comprises an enzyme tag or a magnetic *particle"** tag. ACTIVITY - None given. MECHANISM OF ACTION - Gene therapy. USE - The RCANA are useful for regulating gene expression. It is also useful in assays for detecting the presence of ligands or activation of an effector of RCANA. The nucleic acid is particularly useful in gene therapy. EXAMPLE - Oligos GpIWt3.129 and GpIThlP6.131 were annealed and extended in a 30 microliters reaction containing 100 pmoles of each oligo, 250 mM Tris-HCI, 40 mM MgCl2, 250 mM NaCl, 5 mM DTT, 0.2 mM each dNTO, 45 units of AMV reverse transcriptase at 37 degrees Centigrade for 30 minutes. A polymerase chain reaction (PCR) was thermocycled 20 times under the regime of 94 degrees Centigrade for 30 seconds, 45 degrees Centigrade for 30

seconds, and 72 degrees Centigrade for 1 minute. The PCR reaction was precipitated in the presence of 0.2 M NaCl and 2.5 volumes of ethanol and then quantitated by comparison with a molecular weight standard using agarose gel electrophoresis. The regulatable, catalytically active nucleic acid (RCANA) construct was transcribed in a 10 microl high yield transcription reaction. The reaction contained 500 ng PCR product. The transcription reaction was incubated at 37 degrees Centigrade for 30 minutes. The transcription was then purified on a 6 % denaturing polyacrylamide gel to separate the full length RNA from incomplete transcripts and spliced products, eluted and quantitated spectrophotometrically. 5'-TAA TCT TAC CCC GGA ATT ATA TCC AGC TGC ATG TCA CCA TGA AGA GCA GAC TATATC TCC AAC TTG TTA AAG CAA GTT GTC TAT CGT TTC GAG TCA CTT GAC CCT ACT CCC CAA AGG GAT AGT CGT TAG-3' (GpIWt3.129) 5'-GCC TGAGTA TAA GGT GAC TTA TAC TTG TAA TCT ATC TAA ACG GGG AAC CTC TCT AGT AGA CAA TCC CGT GCT AAA TTA TAC CAG CAT CGT CTT GAT GCC CTT GGC AGA TAA ATG CCT AAC GAC TAT CCC TT-3' (GpITh1P6.131) (126 pages)

14/3,AB/46 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04512174 H.W. WILSON RECORD NUMBER: BGSA01012174
Analysis of proteins and proteomes by mass spectrometry.
Mann, Matthias
Hendrickson, Ronald C; Pandey, Akhilesh
Annual Review of Biochemistry v. 70 (2001) p. 437-73
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 14529

ABSTRACT: A decade after the discovery of electrospray and matrix-assisted laser desorption ionization (MALDI), methods that finally allowed gentle ionization of large biomolecules, mass spectrometry has become a powerful tool in protein analysis and the key technology in the emerging field of proteomics. The success of mass spectrometry is driven both by innovative instrumentation designs, especially those operating on the time-of-flight or ion-trapping principles, and by large-scale biochemical strategies, which use mass spectrometry to detect the isolated proteins. Any human protein can now be identified directly from genome databases on the basis of minimal data derived by mass spectrometry. As has already happened in genomics, increased automation of sample handling, analysis, and the interpretation of results will generate an avalanche of qualitative and quantitative proteomic data. Protein-protein interactions can be analyzed directly by precipitation of a tagged bait followed by mass spectrometric identification of its binding partners. By these and similar strategies, entire protein complexes, signaling pathways, and whole organelles are being characterized. Posttranslational modifications remain difficult to analyze but are starting to yield to generic strategies. Reprinted by permission of the publisher.

14/3,AB/47 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04274000 H.W. WILSON RECORD NUMBER: BGSA00024000

Legionella pneumophila pathogenesis: a fateful journey from amoebae to macrophages.
Swanson, M. S
Hammer, B. K
Annual Review of Microbiology v. 54 (2000) p. 567-613
SPECIAL FEATURES: bibl diag tab ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 21515

ABSTRACT: Legionella pneumophila first commanded attention in 1976, when investigators from the Centers for Disease Control and Prevention identified it as the culprit in a massive outbreak of pneumonia that struck individuals attending an American Legion convention (84). It is now clear that this gram-negative bacterium flourishes naturally in fresh water as a parasite of amoebae, but it can also replicate within alveolar macrophages. L. pneumophila pathogenesis is discussed using the following model as a framework. When ingested by phagocytes, stationary-phase L. pneumophila bacteria establish phagosomes which are completely isolated from the endosomal pathway but are surrounded by endoplasmic reticulum. Within this protected vacuole, L. pneumophila converts to a replicative form that is acid tolerant but no longer expresses several virulence traits, including factors that block membrane fusion. As a consequence, the pathogen vacuoles merge with lysosomes, which provide a nutrient-rich replication niche. Once the amino acid supply is depleted, progeny accumulate the second messenger guanosine 3',5'-bispyrophosphate (ppGpp), which coordinates entry into the stationary phase with expression of traits that promote transmission to a new phagocyte. A number of factors contribute to L. pneumophila virulence, including type II and type IV secretion systems, a pore-forming toxin, type IV pili, flagella, and numerous other factors currently under investigation. Because of its resemblance to certain aspects of Mycobacterium, Toxoplasma, Leishmania, and Coxiella pathogenesis, a detailed description of the mechanism used by L. pneumophila to manipulate and exploit phagocyte membrane traffic may suggest novel strategies for treating a variety of infectious diseases. Knowledge of L. pneumophila ecology may also inform efforts to combat the emergence of new opportunistic macrophage pathogens. Reprinted by permission of the publisher.

14/3,AB/48 (Item 3 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04273994 H.W. WILSON RECORD NUMBER: BGSA00023994
Interim report on genomics of Escherichia coli.
Riley, M
Serres, M. H
Annual Review of Microbiology v. 54 (2000) p. 341-411
SPECIAL FEATURES: bibl tab ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 25680

ABSTRACT: We present a summary of recent progress in understanding Escherichia coli K-12 gene and protein functions. New information has come both from classical biological experimentation and from using the analytical tools of functional genomics. The content of the E. coli genome

can clearly be seen to contain elements acquired by horizontal transfer. Nevertheless, there is probably a large, stable core of >3500 genes that are shared among all E. coli strains. The gene-enzyme relationship is examined, and, in many cases, it exhibits complexity beyond a simple one-to-one relationship. Also, the E. coli genome can now be seen to contain many multiple enzymes that carry out the same or closely similar reactions. Some are similar in sequence and may share common ancestry; some are not. We discuss the concept of a minimal genome as being variable among organisms and obligatorily linked to their life styles and defined environmental conditions. We also address classification of functions of gene products and avenues of insight into the history of protein evolution. Reprinted by permission of the publisher.

14/3,AB/49 (Item 4 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04255643 H.W. WILSON RECORD NUMBER: BGSA00005643
Meiotic chromosomes: integrating structure and function.
AUGMENTED TITLE: review
Zickler, D
Kleckner, N
Annual Review of Genetics v. 33 (1999) p. 603-754
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 73948

ABSTRACT: Meiotic chromosomes have been studied for many years, in part because of the fundamental life processes they represent, but also because meiosis involves the formation of homolog pairs, a feature which greatly facilitates the study of chromosome behavior. The complex events involved in homolog juxtaposition necessitate prolongation of prophase, thus permitting resolution of events that are temporally compressed in the mitotic cycle. Furthermore, once homologs are paired, the chromosomes are connected by a specific structure: the synaptonemal complex. Finally, interaction of homologs includes recombination at the DNA level, which is intimately linked to structural features of the chromosomes. In consequence, recombination-related events report on diverse aspects of chromosome morphogenesis, notably relationships between sisters, development of axial structure, and variations in chromatin status. The current article reviews recent information on these topics in an historical context. This juxtaposition has suggested new relationships between structure and function. Additional issues were addressed in a previous chapter (551). Reprinted by permission of the publisher.

14/3,AB/50 (Item 5 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04045919 H.W. WILSON RECORD NUMBER: BGSA99045919
The 26S proteasome: a molecular machine designed for controlled proteolysis.
Voges, D
Zwickl, P; Baumeister, W
Annual Review of Biochemistry v. 68 (1999) p. 1015-68

SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 23782

ABSTRACT: In eukaryotic cells, most proteins in the cytosol and nucleus are degraded via the ubiquitin-proteasome pathway. The 26S proteasome is a 2.5-MDa molecular machine built from {similar}31 different subunits, which catalyzes protein degradation. It contains a barrel-shaped proteolytic core complex (the 20S proteasome), capped at one or both ends by 19S regulatory complexes, which recognize ubiquitinated proteins. The regulatory complexes are also implicated in unfolding and translocation of ubiquitinated targets into the interior of the 20S complex, where they are degraded to oligopetides. Structure, assembly and enzymatic mechanism of the 20S complex have been elucidated, but the functional organization of the 19S complex is less well understood. Most subunits of the 19S complex have been identified, however, specific functions have been assigned to only a few. A low-resolution structure of the 26S proteasome has been obtained by electron microscopy, but the precise arrangement of subunits in the 19S complex is unclear. Reprinted by permission of the publisher.

14/3,AB/51 (Item 6 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04045895 H.W. WILSON RECORD NUMBER: BGSI99045895
Sterols and isoprenoids: signaling molecules derived from the cholesterol biosynthetic pathway.
Edwards, Peter A
Ericsson, Johan
Annual Review of Biochemistry v. 68 (1999) p. 157-85
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 13161

ABSTRACT: Compounds derived from the isoprenoid/cholesterol biosynthetic pathway have recently been shown to have novel biological activities. These compounds include certain sterols, oxysterols, farnesol, and geranylgeraniol, as well as the diphosphate derivatives of isopentenyl, geranyl, farnesyl, geranylgeranyl, and presqualene. They regulate transcriptional and post-transcriptional events that in turn affect lipid synthesis, meiosis, apoptosis, developmental patterning, protein cleavage, and protein degradation. Reprinted by permission of the publisher.

14/3,AB/52 (Item 7 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03751726 H.W. WILSON RECORD NUMBER: BGSI98001726
Understanding gene and allele function with two-hybrid methods.
Brent, Roger
Finley, Russell L.,Jr
Annual Review of Genetics (Annu Rev Genet) v. 31 ('97) p. 663-704
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English

COUNTRY OF PUBLICATION: United States
WORD COUNT: 16537

ABSTRACT: The use of 2-hybrid systems for detecting protein-protein interactions is reviewed. Use of these systems has enabled the identification of individual important proteins. Recent developments will enable the charting of regulatory networks and the rapid production of hypotheses for the function of genes, allelic variants, and the connections between proteins that constitute these networks. In addition, future developments will enable researchers to test inferences about the role of network elements and permit global approaches to issues relating to biological function.

14/3,AB/53 (Item 8 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03253299 H.W. WILSON RECORD NUMBER: BGSI96003299
Light-harvesting complexes in oxygenic photosynthesis: diversity, control, and evolution.
Grossman, Arthur R
Bhaya, Devaki; Apt, Kirk E
Annual Review of Genetics (Annu Rev Genet) v. 29 ('95) p. 231-88
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 27752

ABSTRACT: The light-harvesting complexes (LHCs) in oxygen-evolving, photosynthetic organisms are reviewed. These organisms include plants, cyanobacteria, diatoms, chrysophytes, dinoflagellates, and red, green, and brown algae. The LHCs represent a diverse range of pigment-protein complexes that facilitate the conversion of radiant energy to chemical bond energy. The synthesis of LHCs is regulated by environmental parameters such as light and nutrients. There are several evolutionary relationships among the LHC structural polypeptides.

14/3,AB/54 (Item 9 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03253297 H.W. WILSON RECORD NUMBER: BGSA96003297
Chlamydomonas reinhardtii as the photosynthetic yeast.
Rochaix, Jean-David
Annual Review of Genetics v. 29 (1995) p. 209-30
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 9815

ABSTRACT: Research on the green unicellular alga Chlamydomonas reinhardtii is reviewed, focusing on the autonomous genetic systems in the nucleus, chloroplast, and mitochondria. Recent technical advances include reliable transformation methods for the 3 genetic compartments, gene tagging, mutant rescue by transformation. Along with classical tools of molecular genetics and biochemistry, these techniques open new areas of research and novel

approaches for investigation. Some such areas of research include chloroplast-mitochondrial interactions, phototransduction, and the behavioral response to light.

14/3,AB/55 (Item 1 from file: 370)
DIALOG(R)File 370:Science

00501181
PTG, a Protein Phosphatase 1-Binding Protein with a Role in Glycogen Metabolism
Printen, John A.; Brady, Matthew J.; Saltiel, Alan R.
J. A. Printen and A. R. Saltiel, Department of Physiology, University of Michigan School of Medicine, Ann Arbor, MI 48109, and Department of Cell Biology, Parke-Davis Pharmaceutical Research Division, Warner-Lambert Company, Ann Arbor, MI 48105, USA. ; M. J. Brady, Department of Cell Biology, Parke-Davis Pharmaceutical Research Division, Warner-Lambert Company, Ann Arbor, MI 48105, USA.
Science Vol. 275 5305 pp. 1475
Publication Date: 3-07-1997 (970307) Publication Year: 1997
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Reports
Word Count: 2338

Abstract: Protein dephosphorylation by phosphatase PP1 plays a central role in mediating the effects of insulin on glucose and lipid metabolism. A PP1C-targeting protein expressed in 3T3-L1 adipocytes (called PTG, for protein targeting to glycogen) was cloned and characterized. PTG was expressed predominantly in insulin-sensitive tissues. In addition to binding and localizing PP1C to glycogen, PTG formed complexes with phosphorylase kinase, phosphorylase a, and glycogen synthase, the primary enzymes involved in the hormonal regulation of glycogen metabolism. Overexpression of PTG markedly increased basal and insulin-stimulated glycogen synthesis in Chinese hamster ovary cells overexpressing the insulin receptor, which do not express endogenous PTG. These results suggest that PTG is critical for glycogen metabolism, possibly functioning as a molecular scaffold.

14/3,AB/56 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

15236795 PASCAL No.: 01-0403998
Receptor-mediated gene transfer by phage-display vectors : applications in functional genomics and gene therapy
LAROCCA David; BAIRD Andrew
Selective Genetics, 11035 Roselle Street, San Diego ,CA 92121, United States
Journal: Drug discovery today, 2001, 6 (15) 793-801
Language: English
Recent studies have demonstrated targeted gene-delivery to mammalian cells using modified phage-display vectors. Specificity is determined by the choice of the genetically displayed targeting ligand. Without targeting, phage *particles"** have virtually no tropism for mammalian

cells. Thus, novel ligands can be selected from phage *libraries"** by their ability to deliver a *reporter"** gene to targeted cells. Together with advances in cDNA display technologies, these findings offer new opportunities for the use of phage-display technology in functional genomics. In addition, targeted phage *particles"** have potential as alternative gene therapy vectors that can be further improved using directed evolution.

14/3,AB/57 (Item 1 from file: 129)
DIALOG(R)File 129:PHIND(Archival)

00584466
European Biotechnology's Sinatra Tribute: We'll Do It Our Way! Highlights of the Sixth Atlas Venture / Ernst and Young European Life Sciences Conference
Bioventure-View 1406 p1, June 01, 1998 (19980601)
STORY TYPE: F WORD COUNT: 7604

- Author(s)

Set	Items	Description
S15	20	AU=(BASIJI, D? OR BASIJI D?)
S16	27	AU=(ORTYN, W? OR ORTYN W?)
S17	16	S15 AND S16
S18	31	S15 OR S16
S19	1	S18 AND S2
S20	15	(S17 OR S19) NOT S12
S21	15	RD (unique items)

>>>No matching display code(s) found in file(s): 129, 229, 453, 624

21/3,AB/1 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

014845050
WPI Acc No: 2002-665756/200271
Related WPI Acc No: 2001-342132; 2001-615235; 2001-647866; 2002-269390; 2002-328950; 2002-426307; 2002-444193; 2002-463279; 2002-489819
XRPX Acc No: N02-526721
Encoded bead decoding method in DNA/RNA analysis, involves dispersing light collected from beads into light beams in accordance with its discriminable characteristics and focusing beams to generate images for analysis
Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; BAUER R A; FINCH R J; FROST K L; *ORTYN W E"**; PERRY D J
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
US 20020094116	A1	20020718	US 2000228076	A	20000825	200271	B
			US 2000240125	A	20001012		
			US 2000242734	A	20001023		
			US 2001976237	A	20011012		

Priority Applications (No Type Date): US 2001976237 A 20011012; US

2000228076 P 20000825; US 2000240125 P 20001012; US 2000242734 P 20001023
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
US 20020094116	A1		49	G06K-009/00	Provisional application US 2000228076
					Provisional application US 2000240125
					Provisional application US 2000242734

Abstract (Basic): US 20020094116 A1
Abstract (Basic):

NOVELTY - The light collected from encoded beads (24) along a collection path, is dispersed into light beams in accordance with discriminable characteristics of the light. The light beams are focused to generate images which are analyzed to determine identity of each encoded bead.

USE - For imaging and decoding encoded reporter labeled beads used for DNA/RNA analysis and analysis of polymorphic allele and single nucleotide polymorphism (SNP).

ADVANTAGE - Enables individual encoded beads to be imaged and the compound attached to the beads to be identified as a function of imaged data. Hence, the identity and sequence of all sub units of the compound are determined effectively.

DESCRIPTION OF DRAWING(S) - The figure shows the isometric view of diagram of imaging apparatus.

Encoded beads (24)

pp; 49 DwgNo 3/27

21/3,AB/2 (Item 2 from file: 351)
DIALOG(R)File 351:Derwent WPI

014669115
WPI Acc No: 2002-489819/200252
Related WPI Acc No: 2001-342132; 2001-615235; 2001-647866; 2002-269390; 2002-328950; 2002-426307; 2002-444193; 2002-463279; 2002-665756
XRAM Acc No: C02-139035

Flow imaging system for collecting image data from encoded beads or for enabling encoded reporter labeled beads to be imaged in stasis or when entrained in a flow of fluid

Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; *ORTYN W E"**; *BASIJI D"**; BAUER R; FINCH R; FROST K; *ORTYN W"**; PERRY D
Number of Countries: 023 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200231182	A2	20020418	WO 2001US42638	A	20011012	200252	B
US 20020071121	A1	20020613	US 99117203	A	19990125	200252	
			US 2000490478	A	20000124		
			US 2000538604	A	20000329		
			US 2000240125	A	20001012		
			US 2001820434	A	20010329		
			US 2001976257	A	20011012		
AU 200211898	A	20020422	AU 200211898	A	20011012	200254	

Priority Applications (No Type Date): US 2001939292 A 20010824; US 2000240125 P 20001012; US 2000242734 P 20001023; US 99117203 P 19990125; US 2000490478 A 20000124; US 2000538604 A 20000329; US 2001820434 A

20010329; US 2001976257 A 20011012
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200231182	A2	E	90	C12Q-000/00	
	Designated States (National): AU CA JP US				
	Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR				
US 20020071121	A1			G01J-003/51	Provisional application US 99117203
					CIP of application US 2000490478
					CIP of application US 2000538604
					Provisional application US 2000240125
					CIP of application US 2001820434
AU 200211898	A			C12Q-000/00	Based on patent WO 200231182

Abstract (Basic): WO 200231182 A2
Abstract (Basic):

NOVELTY - Flow imaging system, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) rapidly imaging and decoding (M1) several encoded beads attached to one or more components associated with one or more reporters where each reporter uniquely identifies a different component;

(2) imaging (M2) several encoded beads entrained in a flow of fluid to identify sequences of components;

(3) simultaneously imaging and identifying (M3) several reporters on different portions of a bead; and

(4) employing an oligo library encoded on beads for at least one of deoxyribonucleic acid (DNA) sequencing, polymorphism analysis, or expression analysis.

USE - The flow imaging system is useful for collecting image data from each encoded bead (claimed). The system is useful for imaging an encoded reporter labeled bead, particularly for enabling encoded reporter labeled beads to be imaged in stasis or when entrained in a flow of fluid.

DESCRIPTION OF DRAWING(S) - The figure shows an imaging system that employs a spectral dispersion filter system comprising several dichroic cube filters oriented at various angles to create the spectral dispersing effect.

fluid flow (22)
images of object (24)
collection lens (32)
imaging lens (40)
optic axis (253)
vertical optic axis (257)
red cube filter (266)
a yellow cube filter (268)
a green cube filter (270)
a TDI detector (274)
optional detector filter assembly (276)
pp; 90 DwgNo 15/27

21/3,AB/3 (Item 3 from file: 351)
DIALOG(R)File 351:Derwent WPI

014642575

WPI Acc No: 2002-463279/200249
Related WPI Acc No: 2001-342132; 2001-615235; 2001-647866; 2002-269390; 2002-328950; 2002-426307; 2002-444193; 2002-489819; 2002-665756
XRAM Acc No: C02-131690
XRPX Acc No: N02-365260
Optically distinct reporter labeled bead construction method involves positioning unique combination of one carrier and one reporter in each reaction vessel
Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; *ORTYN W E"**; *BASIJI D"**; *ORTYN W"**
Number of Countries: 023 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200231501	A1	20020418	WO 2001US42639	A	20011012	200249 B
AU 200211899	A	20020422	AU 200211899	A	20011012	200254
US 20020127603	A1	20020912	US 2000240125	A	20001012	200262
			US 2000242734	A	20001023	
			US 2001976238	A	20011012	

Priority Applications (No Type Date): US 2000242734 P 20001023; US 2000240125 P 20001012; US 2001976238 A 20011012
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200231501	A1	E	33	G01N-033/53	
Designated States (National): AU CA JP US					
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
AU 200211899	A			G01N-033/53	Based on patent WO 200231501
US 20020127603	A1			C12Q-001/68	Provisional application US 2000240125
					Provisional application US 2000242734

Abstract (Basic): WO 200231501 A1
Abstract (Basic):

NOVELTY - Constructing optically distinct reporter labeled bead construction, comprising providing several reaction vessels so that one vessel is available for unique combination of a carrier and reporter, is new. The reporter is attached to the bead by physical and chemical attachments.

USE - For constructing optically distinct reporter labeled beads during combinatorial chemical synthesis.

ADVANTAGE - Reduces number of reporters necessary to encode a library by employing optically distinguishing characteristics for the beads and hence reduces complexity. Reduces number of colors by using intensity characteristics. Reduces number of unique reporters and hence simplifies the task of image analysis of the beads.

DESCRIPTION OF DRAWING(S) - The drawing shows schematic illustration of number of unique pairs and binary codes represented with N unique reporter colors.

pp; 33 DwgNo 2/14

21/3,AB/4 (Item 4 from file: 351)
DIALOG(R)File 351:Derwent WPI

014623489
WPI Acc No: 2002-444193/200247

Related WPI Acc No: 2001-342132; 2001-615235; 2001-647866; 2002-269390; 2002-328950; 2002-426307; 2002-463279; 2002-489819; 2002-665756
XRPX Acc No: NO2-349940
Imaging system for biological samples, has beam splitter which is oriented so that imaged unaltered lights and imaged defocused lights have angular separation other than zero
Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; *ORTYN W E"**; PERRY D J
Number of Countries: 097 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200231583	A1	20020418	WO 2001US31930	A	20011012	200247 B
US 20020051070	A1	20020502	US 2000240125	A	20001012	200247
			US 2001977076	A	20011012	
AU 200213157	A	20020422	AU 200213157	A	20011012	200254

Priority Applications (No Type Date): US 2000240125 P 20001012; US 2001977076 A 20011012
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200231583	A1	E	54	G02B-027/10	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

US 20020051070	A1		H04N-005/232	Provisional application US 2000240125
AU 200213157	A		G02B-027/10	Based on patent WO 200231583

Abstract (Basic): WO 200231583 A1
Abstract (Basic):

NOVELTY - A defocus system (126) modifies the transmitted and reflected lights from a beam splitter (110) as defocused lights. Another beam splitter (114) transmits transmitted and defocused lights and reflects reflected and defocused lights. An imaging lens (118) focuses the transmitted and reflected lights as imaged unaltered lights and the defocused lights as imaged defocused lights. The beam splitter (114) is oriented so that the imaged lights have angular separation other than zero.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for focus maintenance method.

USE - Used for microscopic imaging of biological samples e.g. cell to determine genetic abnormalities or macroscopic imaging of astronomical samples such as stars.

ADVANTAGE - An approximate doubling of optical efficiency is achieved without additional expense and without increasing absorption loss, by utilizing reflectors associated with optical retardation plate. Allows convenient light intensity adjustment and compensation for variation in component efficiencies by using a variable density filter. Provides high resolution image due to defocused light.

DESCRIPTION OF DRAWING(S) - The figure shows the imaging system.
Beam splitters (110,114)
Imaging lens (118)
Defocus system (126)
pp; 54 DwgNo 3/28

21/3,AB/5 (Item 5 from file: 351)
DIALOG(R)File 351:Derwent WPI

014605603
WPI Acc No: 2002-426307/200245
Related WPI Acc No: 2001-342132; 2001-615235; 2001-647866; 2002-269390; 2002-328950; 2002-444193; 2002-463279; 2002-489819; 2002-665756
XRPX Acc No: N02-335197
Cell illumination system has two reflective surfaces defining reflection cavity for light beam
Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; *ORTYN W E"**; *BASIJI D"**; *ORTYN W"**
Number of Countries: 023 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200231467	A1	20020418	WO 2001US42704	A	20011012	200245	B
US 20020057432	A1	20020516	US 2000240125	A	20001012	200245	
			US 2000689172	A	20001012		
			US 2001976465	A	20011012		
AU 200211899	A	20020422	AU 200211899	A	20011012	200254	
AU 200211913	A	20020422	AU 200211913	A	20011012	200254	

Priority Applications (No Type Date): US 2000689172 A 20001012; US 2000240125 P 20001012; US 2001976465 A 20011012; US 2000242734 P 20001023
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200231467	A1	E	51	G01N-001/10	
Designated States (National): AU CA JP US					
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
US 20020057432	A1			G01N-021/05	Provisional application US 2000240125
					CIP of application US 2000689172
AU 200211899	A			G01N-033/53	Based on patent WO 200231501
AU 200211913	A			G01N-001/10	Based on patent WO 200231467

Abstract (Basic): WO 200231467 A1
Abstract (Basic):
NOVELTY - System comprises a light source and two opposed reflecting surfaces defining a reflection cavity so that the light beam is incident on an object traversing the field of view multiple times. Light from the object impinges on a detector but multiply-reflected light does not.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a light collection system;
(2) a flow cytometer system.
USE - System is for battlefield monitoring of airborne toxins and cultured cells to detect the presence of toxins, pre-natal genetic testing and routine cancer screening.
ADVANTAGE - System corrects beam misalignments, improves the signal-to-noise ration and improves measurement consistency.
DESCRIPTION OF DRAWING(S) - The figure shows a beam position and angle detection system used to monitor laser alignment to a cavity.
pp; 51 DwgNo 18/23

21/3,AB/6 (Item 6 from file: 351)
DIALOG(R)File 351:Derwent WPI

014562207
WPI Acc No: 2002-382910/200241
XRPX Acc No: N02-299792
Detector configuration for three dimensional analyses has a time delay integration detector
Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; *ORTYN W E"**; *BASIJI D"**; *ORTYN W"**
Number of Countries: 023 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200217622	A1	20020228	WO 2001US26562	A	20010824	200241	B
US 20020044272	A1	20020418	US 2000228078	P	20000825	200241	
			US 2001932844	A	20010817		
AU 200190573	A	20020304	AU 200190573	A	20010824	200247	

Priority Applications (No Type Date): US 2001932844 A 20010817; US 2000228078 P 20000825
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200217622	A1	E	28	H04N-005/232	
Designated States (National): AU CA JP					
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
US 20020044272	A1			G01N-021/00	Provisional application US 2000228078
AU 200190573	A			H04N-005/232	Based on patent WO 200217622

Abstract (Basic): WO 200217622 A1
Abstract (Basic):
NOVELTY - Light from an object moving through an imaging system is collected, dispersed and imaged onto a time delay integration detector (148). This detector is inclined relative to an axis of motion of the object and produces a pixilated output signal.
DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for a method for determining at least one characteristic of an object
USE - For analyzing three dimensional structures i.e cells
ADVANTAGE - Can tolerate movement of the cells during the imaging process
DESCRIPTION OF DRAWING(S) - The drawing illustrates the focal positioning effects of tilting the TDI detector plane
TDI detector (148)
pp; 28 DwgNo 2/6

21/3,AB/7 (Item 7 from file: 351)
DIALOG(R)File 351:Derwent WPI

014508247
WPI Acc No: 2002-328950/200236
Related WPI Acc No: 2001-342132; 2001-615235; 2001-647866; 2002-269390; 2002-426307; 2002-444193; 2002-463279; 2002-489819; 2002-665756
XRAM Acc No: C02-095012

XRPX Acc No: N02-258187
Imaging system for determining characteristics of object, e.g., cell, comprises collection lens, dispersing component, imaging lens and time delay integration detector
Patent Assignee: BASIJI D A (BASI-I); ORTYN W E (ORTY-I)
Inventor: *BASIJI D A"**; *ORTYN W E"**
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
US 20020030812	A1	20020314	US 99117203	A	19990125	200236 B
			US 2000490478	A	20000124	
			US 2000538604	A	20000329	
			US 2001820434	A	20010329	
			US 2001989031	A	20011121	

Priority Applications (No Type Date): US 99117203 P 19990125; US 2000490478 A 20000124; US 2000538604 A 20000329; US 2001820434 A 20010329; US 2001989031 A 20011121
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
US 20020030812	A1		32	G01J-003/14	Provisional application US 99117203
					CIP of application US 2000490478
					CIP of application US 2000538604
					Cont of application US 2001820434
					CIP of patent US 6211955
					CIP of patent US 6249341

Abstract (Basic): US 20020030812 A1
Abstract (Basic):
NOVELTY - An imaging system comprising:
(a) a collection lens;
(b) a dispersing component;
(c) an imaging lens; and
(d) a time delay integration (TDI) detector, which produces an output signal indicative of characteristic(s) of an object in a broad, flat flow by integrating light from at least a portion of the object over time while the relative movement between the object and the imaging system occurs, is new.
DETAILED DESCRIPTION - An imaging system comprising:
(a) a collection lens with a field angle in an object space that is large enough to collect light traveling from an object that is in a broad, flat flow so that the light passes through the collection lens and travels along a collection path;
(b) a dispersing component disposed in the collection path to receive the light from the object that has passed through the collection lens, where light is dispersed into separate light beams and each light beam is directed away from the dispersing component in a different predetermined direction;
(c) an imaging lens disposed to receive the light beams from the dispersing component, producing images corresponding to each of the light beams, where each image is projected by the imaging lens toward a different predetermined location; and
(d) a time delay integration (TDI) detector disposed to receive the images produced by the imaging lens, producing an output signal that is indicative of characteristic(s) of the object in the broad, flat flow, where the TDI detector produces the output signal by integrating light from at least a portion of the object over time while the relative

movement between the object and the imaging system occurs, is new.
USE - The invention determines morphological, photometric, and spectral characteristics of an object, e.g., cell, in broad, flat flow. It is useful in the analysis of rare cells in the blood for purposes of non-invasive fetal cell diagnosis and cancer screening.
ADVANTAGE - The invention rapidly collects data from a large cell population with high sensitivity and low measurement variation. These data include simultaneous spatial and spectral images covering a large bandwidth at high resolution. The invention further preserves the spatial origin of the spectral information gathered from the object.
DESCRIPTION OF DRAWING(S) - The figure shows an isometric view of an object supported by a slide and moving past a collection lens and a light source in different locations.
Object (24)
Collection lens (32)
Dispersing component (36)
Imaging lens (40)
TDI detector (44)
Light source (62, 64, 66)
pp; 32 DwgNo 7/22

21/3,AB/8 (Item 8 from file: 351)
DIALOG(R)File 351:Derwent WPI

014460271
WPI Acc No: 2002-280974/200232
XRPX Acc No: N02-219418
Time delay integration imaging system for kinetic study of objects using light scattered or emitted from luminescent object to produce image for determining specific characteristics
Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; *ORTYN W E"**; *BASIJI D"**; *ORTYN W"**
Number of Countries: 023 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200216894	A1	20020228	WO 2001US26486	A	20010824	200232	B
US 20020047896	A1	20020425	US 2000228079	P	20000825	200233	
			US 2001932838	A	20010817		
AU 200188385	A	20020304	AU 200188385	A	20010824	200247	

Priority Applications (No Type Date): US 2001932838 A 20010817; US 2000228079 P 20000825
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200216894	A1	E	31	G01J-003/14	
Designated States (National): AU CA JP					
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
US 20020047896	A1			H04N-007/18	Provisional application US 2000228079
AU 200188385	A			G01J-003/14	Based on patent WO 200216894

Abstract (Basic): WO 200216894 A1
Abstract (Basic):
NOVELTY - An imaging system (20) may use a dispersing element (36) to spectrally disperse light at the time delay integration (TDI)

detector so that the kinetics of multiple colors can be analyzed independently, while a shutter (41) or gated image intensifier (43) can be used to obtain a discontinuous image.

DETAILED DESCRIPTION - An object (24), such as a small particle, is carried by a fluid flow (22) through the imaging system and light (30) from the object is focused by lenses onto the TDI detector (44), preferably a charge-coupled device employing a specialized pixel readout algorithm.

AN INDEPENDENT CLAIM is included for a method of determining one of more characteristics of an object using a TDI detector.

USE - Analyzing spectral composition, spatial characteristics and temporal behavior of objects such as cells in motion.

ADVANTAGE - Preventing image blurring of objects in motion.

DESCRIPTION OF DRAWING(S) - The drawing is an isometric view of the system

System (20)
Dispersing element (36)
Shutter (41)
Detector (44)
Object (24)
Flow (22)
pp; 31 DwgNo 1C/7

21/3,AB/9 (Item 9 from file: 351)
DIALOG(R)File 351:Derwent WPI

014448687
WPI Acc No: 2002-269390/200231
Related WPI Acc No: 2001-342132; 2001-615235; 2001-647866; 2002-328950; 2002-426307; 2002-444193; 2002-463279; 2002-489819; 2002-665756
XRPX Acc No: N02-209609
Velocity measurement system for determining indication of velocity of blood cell passing through field of view has light sensitive detector that produces signal responsive to modulated light to determine indication of velocity
Patent Assignee: AMNIS CORP (AMNI-N); BASIJI D A (BASI-I); BAUER R A (BAUE-I); FROST K L (FROS-I); ORTYN W E (ORTY-I); PERRY D J (PERR-I); RILEY J K (RILE-I)
Inventor: *BASIJI D A"**; BAUER R A; FROST K L; *ORTYN W E"**; PERRY D J; RILEY J K; *BASIJI D"**; *ORTYN W"**
Number of Countries: 023 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200217219	A1	20020228	WO 2001US26485	A	20010824	200231	B
AU 200190568	A	20020304	AU 200190568	A	20010824	200247	
US 20020093641	A1	20020718	US 2000228076	A	20000825	200254	
			US 2001939292	A	20010824		
US 20020122167	A1	20020905	US 2000228076	A	20000825	200260	
			US 2001939049	A	20010824		

Priority Applications (No Type Date): US 2000228076 P 20000825; US 2001939292 A 20010824; US 2001939049 A 20010824
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200217219	A1	E	117	G06K-009/00	

Designated States (National): AU CA JP

Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
AU 200190568 A G06K-009/00 Based on patent WO 200217219
US 20020093641 A1 G01P-003/36 Provisional application US 2000228076

US 20020122167 A1 G01P-003/36 Provisional application US 2000228076

Abstract (Basic): WO 200217219 A1
Abstract (Basic):

NOVELTY - A uniform pitch optical grating (46) is disposed in a collection path, for modulating a light traveling along a collection path to produce modulated light having a modulation frequency proportional to a velocity of an object passing through a field of view. A light sensitive detector (50) receives the modulated light and produces a signal responsive to the modulated light. A device processes the signal to determine the indication of the velocity.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for:

(a) a method for determining an indication of a velocity of an object in motion using light from the object

USE - For sensing light from an object with a light sensitive detector and measuring the velocity of the object such as blood cells by analysis of the modulated light signal.

ADVANTAGE - Achieves high precision velocity measurements in an imaging flow cytometer.

DESCRIPTION OF DRAWING(S) - The drawing is a schematic diagram showing the integration of an optical grating into a flow velocity measurement system.

optical grating (46)
light sensitive detector (50)
pp; 117 DwgNo 5/50

21/3,AB/10 (Item 10 from file: 351)
DIALOG(R)File 351:Derwent WPI

014163638
WPI Acc No: 2001-647866/200174
Related WPI Acc No: 2001-342132; 2001-615235; 2002-269390; 2002-328950; 2002-426307; 2002-444193; 2002-463279; 2002-489819; 2002-665756
XRPX Acc No: N01-484112
Imaging system for medical applications has light reflectors positioned at different angles in collection path to reflect light with preset characteristics along different directions
Patent Assignee: BASIJI D A (BASI-I); ORTYN W E (ORTY-I)
Inventor: *BASIJI D A"**; *ORTYN W E"**
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
US 20010021018	A1	20010913	US 99117203	A	19990125	200174	B
			US 2000490478	A	20000124		
			US 2000538604	A	20000329		
			US 2001820434	A	20010329		

Priority Applications (No Type Date): US 99117203 P 19990125; US 2000490478 A 20000124; US 2000538604 A 20000329; US 2001820434 A 20010329
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes

US 20010021018 A1 34 G01J-003/30 Provisional application US 99117203

CIP of application US 2000490478
CIP of application US 2000538604
CIP of patent US 6211955
CIP of patent US 6249341

Abstract (Basic): US 20010021018 A1
Abstract (Basic):
NOVELTY - Light reflectors positioned at different angles with respect to a collection path of imaging system, reflect light of preset characteristics along different directions. The reflectors are adjacently positioned so that light from each of them passes through the preceding reflector, twice.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(a) Light dispersing component;
(b) Object characteristics determining method
USE - For use in medical applications such as non-invasive prenatal genetic testing, routine cancer screening, morphology analysis of moving objects like cells, Fluorescence In-situ Hybridization (FISH) probe detection. For imaging semiconductor wafer, paper etc.
ADVANTAGE - Operates at very high throughput rates with excellent signal to noise ratio by using continuous wave light source. Enables high resolution of the FISH spots by using optical convolution of the narrow band width spectrum resulting in minimal blurring. Prevents overlapping of the field images of various bandwidths on the detector by having nominal angular separation between each bandwidth produced by the spectral dispersing reflectors.
DESCRIPTION OF DRAWING(S) - The figure shows a plan view of spectral dispersion component of stacked dichroic filters for spectral isolation of light.
pp; 34 DwgNo 17/24

21/3,AB/11 (Item 11 from file: 351)
DIALOG(R)File 351:Derwent WPI

014131024
WPI Acc No: 2001-615235/200171
Related WPI Acc No: 2001-342132; 2001-647866; 2002-269390; 2002-328950; 2002-426307; 2002-444193; 2002-463279; 2002-489819; 2002-665756
XRPX Acc No: N01-458853
Moving object imaging system for cells in biological and medical applications, has time delay integration detector to receive image from imaging lens and output signal indicating one characteristic of object
Patent Assignee: AMNIS CORP (AMNI-N)
Inventor: *BASIJI D A"**; *ORTYN W E"**
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
US 6249341	B1	20010619	US 99117203	A	19990125	200171	B
			US 2000490478	A	20000124		

Priority Applications (No Type Date): US 99117203 P 19990125; US 2000490478 A 20000124
Patent Details:

LOCATION: USA
ASSIGNEE: Amnis Corporation
PATENT: U.S. Pat. Appl. Publ. ; US 20020146734 A1 DATE: 20021010
APPLICATION: US 82805 (20020221) *US PV270518 (20010221)
PAGES: 40 pp. CODEN: USXXCO LANGUAGE: English CLASS: 435006000; C12Q-001/68A

21/3,AB/14 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

136320308 CA: 136(21)320308s PATENT
Method and apparatus for reading reporter labeled beads
INVENTOR(AUTHOR): Frost, Keith; Basiji, David; Bauer, Richard; Finch, Rosalynde; Ortyn, William; Perry, David
LOCATION: USA
ASSIGNEE: Amnis Corporation
PATENT: PCT International ; WO 200231182 A2 DATE: 20020418
APPLICATION: WO 2001US42638 (20011012) *US PV240125 (20001012) *US PV242734 (20001023) *US 939292 (20010824)
PAGES: 90 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-000/A
DESIGNATED COUNTRIES: AU; CA; JP; US DESIGNATED REGIONAL: AT; BE; CH; CY ; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; TR

21/3,AB/15 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13202611 BIOSIS NO.: 200100409760
Imaging and analyzing parameters of small moving objects such as cells.
AUTHOR: *Basiji David A"**(a); *Ortyn William E"**
AUTHOR ADDRESS: (a)North Seattle, WA**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office Patents 1247 (3):pNo Pagination June 19, 2001
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Light from an object such as a cell moving through an imaging system is collected and dispersed so that it can be imaged onto a time delay and integration (TDI) detector. The light can be emitted from a luminous object or can be light from a light source that has been scattered by the object or can be a fluorescent emission by one or more FISH probes, frequently used to detect substances within cells. Further, light that is absorbed or reflected by the object can also be used to produce images for determining specific characteristics of the object. The movement of the object matches the rate at which a signal is read from the TDI detector. Multiple objects passing through the imaging system can be imaged, producing both scatter images and spectrally dispersed images at different locations on one or more TDI detectors.

2001

Set Items Description

S22 161 S1 AND (OPTICAL?(5N)SIGNAL?)
S23 7 S22 AND LIBRAR?
S24 6 S23 NOT (S12 OR S20)
S25 6 RD (unique items)
>>>No matching display code(s) found in file(s): 129, 229, 453, 624

25/3,AB/1 (Item 1 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

09083976 Supplier Number: 79197011
39th Annual R&D 100 Awards.(Cover Story)(Industry Overview)
R & D, v43, n9, p29
Sept, 2001
Language: English Record Type: Fulltext
Article Type: Cover Story; Industry Overview
Document Type: Magazine/Journal; Refereed; Trade
Word Count: 23697

25/3,AB/2 (Item 2 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

08654137 Supplier Number: 74925620
GLASS INDUSTRY INDEX.
Glass International, v24, n2, pS37
March, 2001
Language: English Record Type: Fulltext
Document Type: Magazine/Journal; Trade
Word Count: 25154

25/3,AB/3 (Item 3 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

07572707 Supplier Number: 63502067
NEW PRODUCTS.
Lasers & Optronics, v20, n6, p9
June, 2000
Language: English Record Type: Fulltext
Document Type: Tabloid; Academic Trade
Word Count: 8359

25/3,AB/4 (Item 4 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

07039902 Supplier Number: 57162618
AMERICAN COMPANIES IN JAPAN.
Japan-U.S. Business Report, n357, pNA
June, 1999
Language: English Record Type: Fulltext
Document Type: Newsletter; Trade
Word Count: 16446

25/3,AB/5 (Item 1 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01194382 SUPPLIER NUMBER: 08263509 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Product information section. (Clinical Laboratory Reference 1989) (buyers guide)
Medical Laboratory Observer, v21, n13, p16(90)
Annual,
1989
DOCUMENT TYPE: buyers guide PUBLICATION FORMAT: Magazine/Journal ISSN: 0580-7247 LANGUAGE: English RECORD TYPE: Fulltext TARGET AUDIENCE: Academic; Professional
WORD COUNT: 57949 LINE COUNT: 05915

25/3,AB/6 (Item 1 from file: 370)
DIALOG(R)File 370:Science

00505610
Optical Amplification of Ligand-Receptor Binding Using Liquid Crystals
Gupta, Vinay K.; Skaife, Justin J.; Dubrovsky, Timothy B.; Abbott, Nicholas L.
Department of Chemical Engineering and Materials Science, University of California, Davis, CA 95616, USA.
Science Vol. 279 5359 pp. 2077
Publication Date: 3-27-1998 (980327) Publication Year: 1998
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Reports
Word Count: 2874

Abstract: Liquid crystals (LCs) were used to amplify and transduce receptor-mediated binding of proteins at surfaces into optical outputs. Spontaneously organized surfaces were designed so that protein molecules, upon binding to ligands hosted on these surfaces, triggered changes in the orientations of 1-to 20-micrometer-thick films of supported LCs, thus corresponding to a reorientation of ~10.sup(5) to 10.sup(6) mesogens per protein. Binding-induced changes in the intensity of light transmitted through the LC were easily seen with the naked eye and could be further amplified by using surfaces designed so that protein-ligand recognition causes twisted nematic LCs to untwist. This approach to the detection of ligand-receptor binding does not require labeling of the analyte, does not require the use of electroanalytical apparatus, provides a spatial resolution of micrometers, and is sufficiently simple that it may find use in biochemical assays and imaging of spatially resolved chemical
*libraries"**
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